

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2002, 23:48:11 ; Search time 46 Seconds
(without alignments)
4170.430 Million cell updates/sec

Title: US-09-658-824-808

Perfect score: 781

Sequence: 1 gcggcgagctgtgagccgg.....ctttcccccaaaaaaaaaa 781

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	14.1	539	1	US-08-370-648-18
2	110	14.1	539	2	US-08-531-662B-18
3	110	14.1	539	3	US-08-669-161A-18
4	110	14.1	539	3	US-08-602-039-18
5	110	14.1	540	1	US-08-370-648-16
6	110	14.1	540	3	US-08-531-662B-16
7	110	14.1	540	3	US-08-669-161A-16
8	110	14.1	540	3	US-08-602-039-16
9	108.4	13.9	532	2	US-08-370-648-17
10	108.4	13.9	532	2	US-08-531-662B-17
11	108.4	13.9	532	3	US-08-669-161A-17
12	108.4	13.9	532	3	US-08-602-039-17
13	108.4	13.9	538	1	US-08-370-648-14
14	108.4	13.9	538	2	US-08-531-662B-14
15	108.4	13.9	538	3	US-08-669-161A-14
16	108.4	13.9	538	3	US-08-602-039-14
17	108.4	13.9	560	1	US-08-370-648-15
18	108.4	13.9	560	2	US-08-531-662B-15
19	108.4	13.9	560	3	US-08-669-161A-15
20	108.4	13.9	560	3	US-08-602-039-15
21	89.6	11.5	515	4	US-09-439-313-472
22	75.4	9.7	11461	3	US-08-669-161A-29
23	68	8.7	7218	1	US-08-232-463-14
24	58.4	7.5	646	1	US-08-370-648-1
25	58.4	7.5	646	2	US-08-531-662B-1
26	58.4	7.5	646	3	US-08-669-161A-1
27	58.4	7.5	646	3	US-08-602-039-1

Sequence 1, Appli
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 17, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 118, App
Sequence 118, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 14, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl

28 58.4 7.5 648 1 US-08-250-162A-1
29 38 4.9 289 4 US-09-007-005-17
30 38 4.9 289 4 US-09-244-796-17
c 31 36.8 4.7 5288 3 US-08-540-406-18
c 32 36.8 4.7 5288 4 US-08-656-055-18
c 33 36.8 4.7 5288 4 US-08-954-668-18
c 34 36.8 4.7 5288 5 PCT-US95-13233-18
c 35 36 4.6 48974 4 US-08-920-422-17
c 36 34 4.4 43280 2 US-08-804-227C-1
37 33 4.2 3383 1 US-07-707-367-1
38 32.8 4.2 1693 2 US-08-487-113D-118
39 32.8 4.2 1693 2 US-08-720-420A-118
40 32.4 4.1 3251 4 US-09-085-199B-6
41 32 4.1 954 3 US-09-418-641-3
c 42 32 4.1 1437 1 US-08-252-966B-14
43 32 4.1 4695 2 US-08-231-193A-57
44 32 4.1 4695 2 US-08-486-273A-57
45 32 4.1 4695 3 US-08-940-086A-57

ALIGNMENTS

RESULT 1
US-08-370-648-18
; Sequence 18, Application US/08370648
; Patent No. 5648226
; GENERAL INFORMATION:
; APPLICANT: Van den Eynde, Benoit; DeBacker, Olivier;
; APPLICANT: Boon-Falleur, Thierry;
; TITLE OF INVENTION: Isolated, Truncated Nucleic Acid
; TITLE OF INVENTION: Molecules Which Code For GAGE Tumor Rejection Antigen,
; TITLE OF INVENTION: The Tumor Rejection Antigen, and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,648
; FILING DATE: 10-JANUARY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,162
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/096,039
; FILING DATE: 22-JULY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5648226man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5323.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 539 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-370-648-18

Query Match 14.18; Score 110; DB 1; Length 539;
Best Local Similarity 63.9%; Pred. No. 3.6e-25;


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; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/370,648
;   FILING DATE: 10-JANUARY-1995
;   APPLICATION NUMBER: 08/250,162
;   FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/096,039
;   FILING DATE: 22-JULY-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hanson, No. 6069001man D.
;   REGISTRATION NUMBER: 30,946
;   REFERENCE/DOCKET NUMBER: LUD 5323.2
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 688-9200
;   TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 539 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;
US-08-602-039-18

Query Match          14.1%; Score 110; DB 3; Length 539;
Best Local Similarity 63.9%; Pred. No. 3.6e-25;
Matches 216; Conservative 0; Mismatches 115; Indels 7; Gaps 3;

QY 447 CCCCAGGATCAGGTACAGTCCCAAGTCGGGATCTACACCTGGCGACCACACAGAA 506
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Db 202 CCTGAAGAAGGGAACAGCACACTCAACGTGCAGGATCTCGAGCTGCTCAGGAG--GGA 258
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QY 507 GAAGATCAGGATCAGTGCAGATCCCCAGTCGCCGACATGGAAGTGATCTGCAAGAGCTG 566
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Db 259 GAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAG 318
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 567 CATCAGTCAACACCGGGGATTAATCTGGATTGGGTTCGGCGCTCAAGGTGAAGATAAT 626
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Db 319 GGTCACCCACAGACTGGGTGTGAGTGTGAAGAT--GGTCCCTGATGGGAGGTTGGACCC 377
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QY 627 ACCTAAGAGGAACTGTAAAATGCCAAGCAGGTGAAGACGACACCAAGTTTAAAT 686
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Db 378 GCCAATCCAGAGGAGGTGAACGCCCTGAAGAGGTGAAGAGCAATCACAGTGTAAAA 437
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QY 687 GAGACAAGCTGAACAACGCCAGCTGGTTTTATTATTAGATATTG---ACTTAACTAT 743
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 438 GAAGACACGTTGAAATGATCGAGGCTCTCTATGTGGAAATTTGTTCAATTAATTTCT 497
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 744 CTCGAATAAGCTTTGGCAGCTTTCACCAAAAAAAAAAAAA 781
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 498 CCCAATAAGCTTTACAGCCTTCTGCACCAAAAAAAAAAAAA 535
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RESULT 5
US-08-370-648-16
; Sequence 16, Application US/08370648
; Patent No. 5648226
; GENERAL INFORMATION:
; APPLICANT: Van den Eynde, Benoit; DeBacker, Olivier;
; APPLICANT: Boon-Fallieur, Thierry;
; TITLE OF INVENTION: Isolated, Truncated Nucleic Acid
; MOLECULES WHICH CODE FOR GAGE Tumor Rejection Antigen
; MOLECULES WHICH CODE FOR GAGE Tumor Rejection Antigen
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIA TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370.648
FILING DATE: 10-JANUARY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/250.162
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/096.039
FILING DATE: 22-JULY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5648226man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5323.2
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
US-08-370-648-16

Query Match 14.1%; Score 110; DB 1; Length 540;
Best Local Similarity 63.9%; Pred. No. 3.6e-25;
Matches 216; Conservative 0; Mismatches 115; Indels 7; Gaps 3;
QY 447 CCCCCAAAAGAACCCAGCAGCTGAAAGTCGGGATCCTACACCTGGCGCAGCAGACAA 506
DB 203 CTTGAAGAGGGGAACCCAGCACTCAACGTCAGGATCTCGAGCTGCTCAGGAG---GGA 259
QY 507 GAAGATCAGGATACAGCTGAGATCCAGTCGCCGACATGGAAGGTGATCTCAGAGCTG 566
DB 260 GAGGATGAGGAGGAGCTGCGAGGTCAAGGGCCGAAGCTGAAGCTGATAGCCAGGAACAG 319
QY 567 CATCAGTCAAAACACCGGGGATAATCTGGATTTCGGGCTTCCGGCTCAAGGTGAAGATAAT 626
DB 320 GGTCACCCACAGACTGGGTGTGAGTGAAGAT---GGTCTGATGGCGAGGATGGACCC 378
QY 627 ACCTAAGAGGAGCACTGTAAAATGCCAGAGCAGCTGGAAGCAACCAAGTTTAAAT 686
DB 379 GCCAAATCCAGAGGAGGTGAAACGCCCTGAAGAAGGTGAAAGCAATCAACAGTGTAAAA 438
QY 687 GAAGACAAGCTGAACACACCAAGCTGCTTTTATATTAGATATTG---ACTTAAACTAT 743
DB 439 GAAGGCA-GTTGAATGATGCGGCTGCTCTATGTTGGAAATTTGTTCATTTAAATTTCT 498
QY 744 CTCAATAAAGTTTTGCAGCTTTTACCAAAAAA 781
DB 499 CCAATAAAGCTTTACAGCTTCTGCAAAAAA 536

RESULT 6
US-08-531-662B-16
Sequence 16, Application US/08531662B
Patent No. 5858689
GENERAL INFORMATION:
APPLICANT: Van der Bruggen, Pierre;
APPLICANT: Van den Eynde, Benoit; DeBacker, Olivier;
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated, Truncated Nucleic
TITLE OF INVENTION: Acid Molecules Which Code For GAGE Tumor
TITLE OF INVENTION: Rejection Antigen, The Tumor Rejection Antigen,
TITLE OF INVENTION: and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felie & Lynch
STREET: 805 Third Avenue
CITY: New York City

STATE: New York
COUNTRY: USA
ZIP: 10024
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531.662B
FILING DATE: 21-September-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/370.648
FILING DATE: 10-January-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/250.162
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/096.039
FILING DATE: 22-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5858689man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5323.3
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
US-08-531-662B-16

Query Match 14.1%; Score 110; DB 2; Length 540;
Best Local Similarity 63.9%; Pred. No. 3.6e-25;
Matches 216; Conservative 0; Mismatches 115; Indels 7; Gaps 3;
QY 447 CCCCCAAAAGAACCCAGCAGCTGAAAGTCGGGATCCTACACCTGGCGCAGCAGACAA 506
DB 203 CTTGAAGAGGGGAACCCAGCACTCAACGTCAGGATCTCGAGCTGCTCAGGAG---GGA 259
QY 507 GAAGATCAGGATACAGCTGAGATCCAGTCGCCGACATGGAAGGTGATCTCAGAGCTG 566
DB 260 GAGGATGAGGAGGAGCTGCGAGGTCAAGGGCCGAAGCTGAAGCTGATAGCCAGGAACAG 319
QY 567 CATCAGTCAAAACACCGGGGATAATCTGGATTTCGGGCTTCCGGCTCAAGGTGAAGATAAT 626
DB 320 GGTCACCCACAGACTGGGTGTGAGTGAAGAT---GGTCTGATGGCGAGGATGGACCC 378
QY 627 ACCTAAGAGGAGCACTGTAAAATGCCAGAGCAGCTGGAAGCAACCAAGTTTAAAT 686
DB 379 GCCAAATCCAGAGGAGGTGAAACGCCCTGAAGAAGGTGAAAGCAATCAACAGTGTAAAA 438
QY 687 GAAGACAAGCTGAACACCAAGCTGCTTTTATATTAGATATTG---ACTTAAACTAT 743
DB 439 GAAGGCACTGTTGAATGATGCGGCTGCTCTATGTTGGAAATTTGTTCATTTAAATTTCT 498
QY 744 CTCAATAAAGTTTTGCAGCTTTTACCAAAAAA 781
DB 499 CCAATAAAGCTTTACAGCTTCTGCAAAAAA 536

RESULT 7
US-08-669-161A-16
Sequence 16, Application US/08669161A
Patent No. 6013481
GENERAL INFORMATION:
APPLICANT: DeBacker, Olivier; Van den Eynde,
APPLICANT: Benoit; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated, Truncated Nucleic Acid


```

: TITLE OF INVENTION: Molecules Which Code For GAGE Tumor Rejection Antigen,
: TITLE OF INVENTION: The Tumor Rejection Antigen, and Uses thereof
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Felfe & Lynch
: STREET: 805 Third Avenue
: CITY: New York City
: STATE: New York
: COUNTRY: USA
: ZIP: 10022
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: PC-DOS
: SOFTWARE: Wordperfect
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/669,161A
: FILING DATE: 24-June-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/531,662
: FILING DATE: 21-September-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/370,648
: FILING DATE: 10-January-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/250,162
: FILING DATE: 27-May-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/096,039
: FILING DATE: 22-July-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Hanson, No. 6013481man D.
: REGISTRATION NUMBER: 30,946
: REFERENCE/DOCKET NUMBER: LUD 5443
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 688-9200
: TELEFAX: (212) 838-3884
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 540 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-08-669-161A-16

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RESULT 8
 US-08-602-039-16
 : Sequence 16, Application US/08602039
 : Patent No. 6069001
 : GENERAL INFORMATION:
 : APPLICANT: Van den Eynde, Benoit; DeBacker, Olivier;
 : APPLICANT: Boon-Falleur, Thierry;
 : TITLE OF INVENTION: Isolated, Truncated Nucleic Acid
 : TITLE OF INVENTION: Molecules Which Code For GAGE Tumor Rejection Antigen,
 : TITLE OF INVENTION: The Tumor Rejection Antigen, and Uses Thereof
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Felfe & Lynch
 : STREET: 805 Third Avenue
 : CITY: New York City
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10022
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 : COMPUTER: IBM PS/2
 : OPERATING SYSTEM: PC-DOS
 : SOFTWARE: Wordperfect
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/602,039
 : FILING DATE: 15-FEB-1996
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/370,648
 : FILING DATE: 10-JANUARY-1995
 : APPLICATION NUMBER: 08/250,162
 : FILING DATE: 27-MAY-1994
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/096,039
 : FILING DATE: 22-JULY-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Hanson, No. 6069001man D.
 : REGISTRATION NUMBER: 30,946
 : REFERENCE/DOCKET NUMBER: LUD 5323.2
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212) 688-9200
 : TELEFAX: (212) 838-3884
 : INFORMATION FOR SEQ ID NO: 16:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 540 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 US-08-602-039-16


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Qy 507 GAAGATCAGGATACAGCTGAGATCCAGTCCGCGACATGGAAGGTGATCTGCAAGACCTG 566
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Db 252 GAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCTCAAGCTGATAGCCAGGAACAG 311
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 567 CATCAGTCAACACCCGGGATAACTCGGATTTGGGTTCCGGCTCAAGGTGAAGATAAT 626
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 312 GGTCAACCCAGAGTGGGTGAGTGGAAGAT--GGTCCTGATGGCGGAGGATGGACCC 370
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 627 ACCTAAAGAGGAACTGTAAAATGCCAGAGCGAGGTGAAGAGCAACCAAGTTTAAAT 686
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Db 371 GCCAAATCCAGAGAGGTGAAACGCCCTGAAGAGGTGAAAAGCAATCACAGTCTTAAA 430
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 687 GAAGACAAGCTGAACACCAAGCTGGTTTATATATAGATATTTG---ACTTAAACTAT 743
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 431 GAAGCAGCTTGAATGATCAGGCTGCTCTATGTTGGAATTTGTTCAATAAATCT 490
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 744 CTCATAAAGTTTGCAGCTTTCACCAAAAAA 781
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 491 CCCAATAAGCTTTACAGCCTTCTGCAAGAAAAA 528
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RESULT 11
US-08-669-161A-17
; Sequence 17, Application US/08669161A
; Patent No. 6013481
; GENERAL INFORMATION:
; APPLICANT: DeBacker, Olivier; Van den Eynde,
; APPLICANT: Benoît; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated, Truncated Nucleic Acid
; TITLE OF INVENTION: Molecules Which Code For GAGE Tumor Rejection Antigen,
; TITLE OF INVENTION: The Tumor Rejection Antigen, and Uses Thereof
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,161A
; FILING DATE: 24-June-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/531,662
; FILING DATE: 21-September-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/370,648
; FILING DATE: 10-January-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,162
; FILING DATE: 27-May-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/096,039
; FILING DATE: 22-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6013481man D.
; REGISTRATION NUMBER: 30,946
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-08-669-161A-17
Query Match 13.9%; Score 108.4; DB 3; Length 532;
Best Local Similarity 63.6%; Pred. No. 1.1e-24;
Matches 215; Conservative 0; Mismatches 116; Indels 7; Gaps 3;

Qy 447 CCCCCAAAAGAAAGAACAGCAGCTGAAAGTGGGATCTACACCTGGGCGACAGACAGAA 506
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 195 CCTGAAGAGGGAACACAGCAACTCAACGTCCAGCTCCTGCAGCTGCTCAGGAG---GGA 251
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 507 GAAGATCAGGATACAGCTGAGATCCCAGTCCGCGACATGGAAGGTGATCTGCAAGACCTG 566
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 252 GAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCTCAAGCTGATAGCCAGGAACAG 311
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 567 CATCAGTCAACACCCGGGATAAATCTGGATTTGGGTTCCGGCTCAAGGTGAAGATAAT 626
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 312 GGTCAACCCAGAGTGGGTGAGTGGAAGAT--GGTCCTGATGGCGGAGGATGGACCC 370
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 627 ACCTAAAGAGGAACTGTAAAATGCCAGAGCGAGGTGAAGAGCAACCAAGTTTAAAT 686
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 371 GCCAAATCCAGAGAGGTGAAACGCCCTGAAGAGGTGAAAAGCAATCACAGTCTTAAA 430
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 687 GAAGACAAGCTGAACACCAAGCTGGTTTATATATAGATATTTG---ACTTAAACTAT 743
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 431 GAAGCAGCTTGAATGATCAGGCTGCTCTATGTTGGAATTTGTTCAATAAATCT 490
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 744 CTCATAAAGTTTGCAGCTTTCACCAAAAAA 781
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 491 CCCAATAAGCTTTACAGCCTTCTGCAAGAAAAA 528
    ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-08-602-039-17
; Sequence 17, Application US/08602039
; Patent No. 6069001
; GENERAL INFORMATION:
; APPLICANT: Van den Eynde, Benoît; DeBacker, Olivier;
; APPLICANT: Boon-Falleur, Thierry;
; TITLE OF INVENTION: Isolated, Truncated Nucleic Acid
; TITLE OF INVENTION: Molecules Which Code For GAGE Tumor Rejection Antigen,
; TITLE OF INVENTION: The Tumor Rejection Antigen, and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,039
; FILING DATE: 15-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/370,648
; FILING DATE: 10-JANUARY-1995
; APPLICATION NUMBER: 08/250,162
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/096,039
; FILING DATE: 22-JULY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6069001man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5323.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
```

```
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-602-039-17

Query Match          13.9%; Score 108.4; DB 3; Length 532;
Best Local Similarity 63.6%; Pred. No. 1.1e-24;
Matches 215; Conservative 0; Mismatches 116; Indels 7; Gaps 3;

Qy 447 CCCAAAAGAGAACCCAGCAGCTGAAAGTCGGGATCCTACACCTGGCGACAGAGAA 506
   || || || || || || || || || || || || || || || || || || || ||
Db 195 CCGTGAAGAGGGGACACCAAGCACTCAACGTCAGGATCCTGCAGCTGCTCAGGAG 251

Qy 507 GAAGATCAGGATACAGCTGAGATCCAGTCAGTCGCGACATGGAAGGTGATCTGCAAGAGCTG 566
   || || || || || || || || || || || || || || || || || || || ||
Db 252 GAGGATGAGGAGGAGCTGCGAGGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGAACAG 311

Qy 567 CATCAGTCAACACACCGGGGATAAATCTGGATTGGGTTCCGGCGTCAAGGTGAAGATAAT 626
   || || || || || || || || || || || || || || || || || || || ||
Db 312 GGTCAACCCACAGACTGGGTGTGAGTGTGAAGAT -GGTCTGTATGGCAGGAGATGGACCC 370

Qy 627 ACCTAAGAGGACACTGTAAATGCCAGACAGCTGAAGAGCAACCAAGTTTAAT 686
   || || || || || || || || || || || || || || || || || || || ||
Db 371 GCCAATCCAGAGGAGGTGAAACGCCCTGAAGAGGTGAAAGCAATCACAGTGTAAAA 430

Qy 687 GAAGACAAGCTGAAACAACGCAAGCTGGTGTATATATAGATATTG---ACTTAAACTAT 743
   || || || || || || || || || || || || || || || || || || || ||
Db 431 GAAGCACGTTGAAATGATGAGGCTGCTCTATCTTGGAAATTTGTTCAATTAATTTCT 490

Qy 744 CTCATAAAGTTTTCAGCTTTCACCAAAAAA 781
   || || || || || || || || || || || || || || || || || || || ||
Db 491 CCCAATAAGCTTTACAGCCTTCTGCAAAAGAAAAA 528

RESULT 13
US-08-370-648-14
; Sequence 14, Application US/08370648
; Patent No. 5648226
; GENERAL INFORMATION:
; APPLICANT: Van den Eynde, Benoit; DeBacker, Olivier;
; APPLICANT: Boon-Falleur, Thierry;
; TITLE OF INVENTION: Isolated, Truncated Nucleic Acid
; TITLE OF INVENTION: Molecules Which Code For GAGE Tumor Rejection Antigen,
; TITLE OF INVENTION: The Tumor Rejection Antigen, and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,648
; FILING DATE: 10-JANUARY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,162
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/096,039
; FILING DATE: 22-JULY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5648226man D.
; REGISTRATION NUMBER: 30,946
```

```
; REFERENCE/DOCKET NUMBER: LUD 5323.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 538 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-370-648-14

Query Match          13.9%; Score 108.4; DB 1; Length 538;
Best Local Similarity 63.6%; Pred. No. 1.1e-24;
Matches 215; Conservative 0; Mismatches 116; Indels 7; Gaps 3;

Qy 447 CCCAAAAGAGAACCCAGCAGCTGAAAGTCGGGATCCTACACCTGGCGACAGAGAA 506
   || || || || || || || || || || || || || || || || || || || ||
Db 201 CCGTGAAGAGGGGACACCAAGCACTCAACGTCAGGATCCTGCAGCTGCTCAGGAG---GGA 257

Qy 507 GAAGATCAGGATACAGCTGAGATCCAGTCAGTCGCGACATGGAAGGTGATCTGCAAGAGCTG 566
   || || || || || || || || || || || || || || || || || || || ||
Db 258 GAGGATGAGGAGGAGCTGCGAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAG 317

Qy 567 CATCAGTCAACACACCGGGGATAAATCTGGATTGGGTTCCGGCGTCAAGGTGAAGATAAT 626
   || || || || || || || || || || || || || || || || || || || ||
Db 318 GGTCAACCCACAGACTGGGTGTGAGTGTGAAGAT -GGTCTGTATGGCAGGAGATGGACCC 376

Qy 627 ACCTAAGAGGAGCACTGTAAATGCCAGACAGCTGAAGAGCAACCAAGTTTAAT 686
   || || || || || || || || || || || || || || || || || || || ||
Db 377 GCCAATCCAGAGGAGGTGAAACGCCCTGAAGAGGTGAAAGCAATCACAGTGTAAAA 436

Qy 687 GAAGACAAGCTGAAACAACGCAAGCTGGTGTATATATAGATATTG---ACTTAAACTAT 743
   || || || || || || || || || || || || || || || || || || || ||
Db 437 GAAGACAGCTTGAATGATGAGGCTGCTCTATCTTGGAAATTTGTTCAATTAATTTCT 496

Qy 744 CTCATAAAGTTTTCAGCTTTCACCAAAAAA 781
   || || || || || || || || || || || || || || || || || || || ||
Db 497 CCCAATAAGCTTTACAGCCTTCTGCAAAAGAAAAA 534

RESULT 14
US-08-531-662B-14
; Sequence 14, Application US/08531662B
; Patent No. 5858689
; GENERAL INFORMATION:
; APPLICANT: Van der Bruggen, Pierre;
; APPLICANT: Van den Eynde, Benoit; DeBacker, Olivier;
; APPLICANT: Boon-Falleur, Thierry;
; TITLE OF INVENTION: Isolated, Truncated Nucleic
; TITLE OF INVENTION: Acid Molecules Which Code For GAGE Tumor
; TITLE OF INVENTION: Rejection Antigen, The Tumor Rejection Antigen,
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,662B
; FILING DATE: 21-September-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/370,648
; FILING DATE: 10-January-1995
```


Query Match	8.7%	Score 68;	DB 1;	Length 7218;
Best Local Similarity	3.6%;	pred. NO.	3.2e-11;	
Matches	14;	Conservative	233;	Mismatches 142; Indels 0; Gaps 0;
QY	340	GACAGAGAATCTGGACTCCCGACACGCGGACCAGGAGGAGCGGCATGACCCACACACA	399	
Db	1452	GATAGAAGAATTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	1393	
		: : : : : : : : : :		
QY	400	CAAAACACAGAACACACAGCAGTCGCCAGGAGCCAGCTAATGGAGAGCCCCAAAACAG	459	
		: : : : : : : : : :		
Db	1392	RRR	1333	
		: : : : : : : : : :		
QY	460	AACCACAGCTGAAGTCGGGTACCTACACTGGGAGCACAGACAGAGCATCAGGATA	519	
		: : : : : : : : : :		
Db	1332	RRR	1273	
		: : : : : : : : : :		
QY	520	CAGCTGAGATCCCAGTCGCGCGACATGCAAGTGATCTGCAAGAGCTCATCAGTCAACA	579	
		: : : : : : : : : :		
Db	1272	RRR	1213	
		: : : : : : : : : :		
QY	580	CCGGGATAAATCTGGATTGGTTCCGGCGTCAAGGTGAAGATAATACCTTAAGAGGAA	639	
		: : : : : : : : : :		
Db	1212	RRR	1153	
		: : : : : : : : : :		
QY	640	CAGTGTAAAAATGCCAGAAGCAGGTGAAGAGCAACCAAGCTTTAAATGAAGACAAGCTGA	699	
		: : : : : : : : : :		
Db	1152	RRR	1093	
		: : : : : : : : : :		
QY	700	AACAACCGAAGCTGGTTTTATATVAGAT	727	
		: : : : : : : : : :		
Db	1092	RRR	1065	
		: : : : : : : : : :		

RESULT 24
US-08-370-648-1
; Sequence 1, Application US/08370648
; Patent No. 5648226
; GENERAL INFORMATION:
; APPLICANT: Van den Eynde, Benoit; DeBacker, Olivier;
; APPLICANT: Boon-Fallieur, Thierry;
; TITLE OF INVENTION: Isolated, Truncated Nucleic Acid
; TITLE OF INVENTION: Molecules Which Code For GAGE Tumor Rejection Antigen,
; TITLE OF INVENTION: The Tumor Rejection Antigen, and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felre & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,648
; FILING DATE: 10-JANUARY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,162
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/096,039
; FILING DATE: 22-JULY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No 5648226man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5323.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200

```

; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 646 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-370-648-1

Query Match 7.5%; Score 58.4; DB 1; Length 646;
Best Local Similarity 70.5%; Pred. No. 8.5e-09;
Matches 93; Conservative 0; Mismatches 36; Indels 3; Gaps

QY 653 CAGAAGCAGGTGAAGACCAACCACCAAGTTTAAATGAAGACAAGCTGAAACACGCGAAGCT 712
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 511 CTGTGGCATGTGAAGGCAATACACAGTGTAAAAAGAAGACATCTGAAATGTGTGCAGGCT 570
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 713 GGTTTTATTAGATATTTC---ACTTAAACTATCTCAATAAAAGTTTTTCAGCTTTTCACC 769
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 571 GCTCCTATGTGGAAATCTTTCATTCAAGCTTCTCCCAATAAGCTTTACAGGCTTCTGC 630
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 770 AAAAAAAAAA 781
   | | | | | | | | | |
Db 631 AAAAAAAAAA 642

RESULT 25
US-08-531-662B-1
; Sequence 1, Application US/08531662B
; Patent No. 5858689
; GENERAL INFORMATION:
; APPLICANT: Van der Bruggen, Pierre;
; APPLICANT: Van den Eynde, Benoit; DeBacker, Olivier;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated, Truncated Nucleic
; TITLE OF INVENTION: Acid Molecules Which Code For GAGE Tumor
; TITLE OF INVENTION: Rejection Antigen, The Tumor Rejection Antigen,
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,662B
; FILING DATE: 21-September-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/370,648
; FILING DATE: 10-January-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,162
; FILING DATE: 27-May-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/096,039
; FILING DATE: 22-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5858689man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5323.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

```



```

; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

Query Match
Best Local Similarity 4.9%; Score 38; DB 4; Length 289;
Matches 12; Conservative 97; Mismatches 109; Indels 0; Gaps 0;

Qy 347 GATTCTGGACTCCCGACAGCGGACGAGGAGCGGCATGAGCGACACACAAACAC 406
Db 25 RARURURARCRARURURARCRARURGRNRRNRRNRRNRRNRRNRRNRRN 84
Qy 407 AGAACACACAGCGCCCGAGGAGCCCGAGTATGGAGAGCCCGCCAAAGAACACGC 466
Db 85 RSRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRN 144
Qy 467 AGCTGAAAGTCGGATCTACACCTCGGCGACAGACAGAGAGATCAGGATACAGCTGA 526
Db 145 RSRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRN 204
Qy 527 GATCCAGTCGCGGACATCGGAAGTGATCTGCAAGAGC 564
Db 205 RSRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRNRRN 242

RESULT 31
US-08-540-406-18/c
; Sequence 18, Application US/08540406
; Patent No. 5837538
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-540-406-18

Query Match
Best Local Similarity 4.9%; Score 36.8; DB 3; Length 5288;
Matches 80; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 630 TAAAGAGGAACACTGTAAATGCCAGAGCAGGTTGATATGCAATTTAAATGAA 689
Db 5222 TTAACAGTAACATTTTCAATACCTATTACATAAGCAATATTTGCATAGAAATTATACAAGT 5103
```

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; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-540-406-18

Query Match
Best Local Similarity 4.7%; Score 36.8; DB 2; Length 5288;
Matches 80; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 630 TAAAGAGGAACACTGTAAATGCCAGAGCAGGTTGATATGCAATTTAAATGAA 689
Db 5222 TTAACAGTAACATTTTCAATACCTATTACATAAGCAATATTTGCATAGAAATTATACAAGT 5103

Qy 690 GACAAGCTGAACACACGCGAGCTGTTTATATTTAGATATTTGACTTAAACTATCTCAAT 749
Db 5162 CAGAAACCTTTACAAAATAATCCTATTACATAAGCAATATTTGCATAGAAATTATACAAGT 5103

Qy 750 AAAGTTTTGCAGCTTTCACCAAAAAA 781
Db 5102 AAATTATACAATATTTAAGCAGCAGCAACATA 5071

RESULT 32
US-08-656-055-18/c
; Sequence 18, Application US/0856055
; Patent No. 6027882
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,055
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/540,406
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-656-055-18

Query Match
Best Local Similarity 4.7%; Score 36.8; DB 3; Length 5288;
Matches 80; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 630 TAAAGAGGAACACTGTAAATGCCAGAGCAGGTTGATATGCAATTTAAATGAA 689
Db 5222 TTAACAGTAACATTTTCAATACCTATTACATAAGCAATATTTGCATAGAAATTATACAAGT 5103
```

Qy	690	GACAAGCTGAAACAAACGCAAGCTGCTTTATATTAGATATTTGACTTTAAACATCTCTCAAT	749
Db <td>5162</td> <td>CAGAAACCTTTACAAAATAATCCTATTACATAAGCAATATTTGCATACGAATTATACAAGT</td> <td>5103</td>	5162	CAGAAACCTTTACAAAATAATCCTATTACATAAGCAATATTTGCATACGAATTATACAAGT	5103
Qy <td>750</td> <td>AAAGTTTTTCAGCTTTTCACCAAAAAAAAAAAAA</td> <td>781</td>	750	AAAGTTTTTCAGCTTTTCACCAAAAAAAAAAAAA	781
Db <td>5102</td> <td>AAATTATACAATATTTTAAGCAGCAGCAACATA</td> <td>5071</td>	5102	AAATTATACAATATTTTAAGCAGCAGCAACATA	5071

```

RESULT 33
US-08-954-668-18/c
; Sequence 18, Application US/08954668
; Patent No. 6172200
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GODDRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

```

Query Match	4.7%	Score 36.8	DB 4	Length 5288
Best Local Similarity	52.6%	Pred. No. 0.2		
Matches	80	Conservative	Mismatches	72
			Indels	0
			Gaps	0
QY 630	TAAACAGCAACACTCT	AAATGCCAGAAAGCAGGTTGAAGACGCAACACAGTTTAAATGAA	689	
Db 5222	TTACACGTAACATTT	CATCTACATACCACAGGTTTGTATGTCAAATTTAAATATTTTAAA	5163	
QY 690	GACAAGCTGAAACACGCA	AGCTGGTTTTATATATAGATATTTGACCTTAAACTATCTCTCAAT	749	
Db 5162	CAGAAACCTTTTACAA	AAATCTCTTACATAGCAATATTTGCATAGATTTATACAAGT	5103	
QY 750	AAAGTTTTGCAGCTTTC	CACCAAAAAA	781	
Db 5102	AAATATACAATATTT	TAAGCAGCGACCAACATA	5071	

RESULT 34
PCT-US95-13233-18/c
; Sequence 18, Application PC/TUS9513233
; GENERAL INFORMATION:

```

: APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY
:
: TITLE OF INVENTION: Patched Genes and their Use
:
: NUMBER OF SEQUENCES: 19
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
:
: STREET: Four Embarcadero Center, Suite 3400
:
: CITY: San Francisco
:
: STATE: CA
:
: COUNTRY: US
:
: ZIP: 94111
:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: PCT/US95/13233
:
: FILING DATE: 06-OCT-1990
:
: CLASSIFICATION:
:
: ATTORNEY/AGENT INFORMATION:
:
: NAME: Rowland, Bertram I
:
: REGISTRATION NUMBER: 20015
:
: REFERENCE/DOCKET NUMBER: a60190-1
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: 415-781-1989
:
: TELEFAX: 415-398-3249
:
: INFORMATION FOR SEQ. ID NO.: 18:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 5288 base pairs
:
: TYPE: nucleic acid
:
: STRANDEDNESS: single
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: cDNA
:
: PCT-US95-13233-18

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	Query Match	4.7%;	Score 36.8;	DB 5;	Length 5288;
	Best Local similarity	52.6%;	Pred. No. 0.2;		
	Matches	80;	Conservative	0;	Mismatches 72; Indels 0; Gaps 0;
QY	630	TAAGAGGAACTGTAAATGCGAGAAGCAGCGTGAAGACGACACCAAGT	TTTTAAATGAA	689	
Db	5222	TTAACAGTAACATTTATACCTACCAAGGGTGTGATATGCAAAATTTAA	AAATATTTTAA	5163	
QY	690	GACAAGCTGAACAACGCAAGCTGGTTTATATAGATATTTGACCTTAA	CAATCTCAAT	749	
Db	5162	CAGAACCCITTACAAATAATCCTATTACATAAGCAATATTTGCATAGA	ATTTATACAAGT	5103	
QY	750	AAAGTTTTGGAGCTTTTACACCAAAAAA	AAAAA	781	
Db	5102	AAATTTATACAATATTTTAAAGCAGCAGCAACATA		5071	

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RESULT 35
US-08-920-422-17/c
; Sequence 17, Application US/08920422A
; Patent No. 6255473
; GENERAL INFORMATION:
; APPLICANT: Vitek, Michael P.
; APPLICANT: Mitsuda, No. 6255473iaki
; APPLICANT: Roses, Allen D.
; TITLE OF INVENTION: Presenilin-1 Gene Promoter
; FILE REFERENCE: VITEKPRESNILIN
; CURRENT APPLICATION NUMBER: US/08/920,422A
; CURRENT FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 17
; LENGTH: 48974
; TYPE: DNA
; ORGANISM: Mus musculus
US-08-920-422-17

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Query Match 4.6%; Score 36; DB 4; Length 48974;


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; INDIVIDUAL ISOLATE: precursor to PHL enzyme
; IMMEDIATE SOURCE:
; CLONE: PAE-III-202-4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..2835
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1177..2145
US-07-707-367-1
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Query Match          4.2%; Score 33; DB 1; Length 3383;
Best Local Similarity 54.5%; Pred. No. 2.5;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 443 AGAGCCCCAAAAGAAAGAACAGACAGCTGAAGTCCGGATCCTACACCTGGCGGACGAC 502
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2316 AGAAGCAAGCAAAATGTTGCAAGAGATCAATGCTGGGGTGCTACACAAGAGACGAA 2375

QY 503 AGAAGAAGATCAGGATACAGTCAGATCCCAAGTCCGCGACATGGAAGGTGATCTGCAAGA 562
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2376 TCTTGTGCAAGAGAGTAGTGTCTGGGTGCTCTACACAGAGAGAGAGAGTGTGTGCAAGA 2435

QY 563 G 563
DB 2436 G 2436
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RESULT 38
US-08-487-113D-118
; Sequence 118, Application US/08487113D
; Patent No. 5837822
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,113D
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5837822and, Greta E.
```

```
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1693 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1587
US-08-487-113D-118

Query Match          4.2%; Score 32.8; DB 2; Length 1693;
Best Local Similarity 56.5%; Pred. No. 1.9;
Matches 61; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 301 TGTGGGGGTATCCGAGTCCAGAAAGCACCTGGAAACCCCGACAGAAAGATTCTGCACCTCCC 360
      |||| | | ||||| |||| | | |||| | | |||| | | |||| | | |||| | | ||||
DB 689 TGTTCGCCGCTCGAGGCCCAAGTCCACTTGGCGCTGGGGAACCCAGACGCTGAACCTTA 748

QY 361 CACAGGGGACAGGAGAGGGGACGCGCATGAGGACACACACACAAACACAG 408
      |||| | | || | | | | | | | | | | | | | | | | | | | | | | | | |
DB 749 CAGTCGAGAGCCAGCGGGGACACGATCAGTGCCA'AGCCACAGGCGGTAG 796

RESULT 39
US-08-720-420A-118
; Sequence 118, Application US/08720420A
; Patent No. 5989843
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,420A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,113
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
```



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;
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Joseph A., Jr.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 33282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1693 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1587
; US-08-720-420A-118

Query Match 4.2%; Score 32.8; DB 2; Length 1693;
Best Local Similarity 56.3%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 47;

QY 301 TGTTCGGGGTATCGAGTCCCGAGAGCAGCCTGGAAACCCCGACAGAGATTCTGGACTCC 360
Db 689 TGTTCGGGCTCGGAGGCCCAAGTCCACTTGGCGGTGGGGAACCGACAGACCTGAACCTCTA 748

QY 361 CAGACGGGACCGAGAGGAGCGCATCAGCGACACACACAAACACAG 408
Db 749 CAGTCGAGAGCCAGCGGGACACGATCATGTCACGACGACGCGGTAG 796

RESULT 40
US-09-085-199B-6
; Sequence 6, Application US/09085199B
; Patent No. 6235679
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Hackam, Abigail
; APPLICANT: Huq, A.H.M. Mahbubul
; APPLICANT: Chopra, Vikramjit Singh
; APPLICANT: Kalchman, Michael
; TITLE OF INVENTION: Apoptosis Modulators That Interact with the
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: PO Box 5270
; CITY: Frisco
; STATE: CO
; COUNTRY: USA
; ZIP: 80443-5270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS DOS 5.0
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,199B
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32038
; REFERENCE/DOCKET NUMBER: UBC.P-0130S2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 668-2050
; TELEFAX: (970) 668-2052
;
```

```
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3251
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: cDNA for Huntington-interacting protein
; US-09-085-199B-6

Query Match 4.1%; Score 32.4; DB 4; Length 3251;
Best Local Similarity 54.1%; Pred. No. 3.7;
Matches 66; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 488 ACCTGGCGACGACAGACAGAAAGATCAGGATACAGCTGAGATCCCAGTGGCGGACATGGA 547
Db 508 AGCTGTGCGGCGAGCGGAGGACAGACCTGCTGGCGGCGAGAGCCTGGTGGCGGAGACAGA 567

QY 548 AGCTGATCTGCAAGAGCTGCATCAGTCAAAACACGGGGATAAATCTGGATTTCGGTTCCG 607
Db 568 GGCGCGCTGAGCCGGAGCAGCAGCCAGCTCCAGGACGAGGCGGAGTTGCGAGGCGCG 627

QY 608 GC 609
Db 628 GC 629
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Search completed: October 17, 2002, 00:58:28
Job time : 102 s r v s

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c 221	19	2.4	134506	9	HS357116	AL021921 Homo sapi
c 222	19	2.4	135144	9	AC093248	AC093248 Homo sapi
c 223	19	2.4	135671	2	AC107529	AC107529 Rattus no
c 224	19	2.4	136963	2	AC084817	AC084817 Rattus sat
c 225	19	2.4	136943	9	AL359842	AL359842 Human DNA
c 226	19	2.4	137063	9	AC021086	AC021086 Homo sapi
c 227	19	2.4	137229	9	AC010877	AC010877 Homo sapi
c 228	19	2.4	137592	9	AC008625	AC008625 Homo sapi
c 229	19	2.4	138329	2	AC093226	AC093226 Homo sapi
c 230	19	2.4	138414	2	AC008798	AC008798 Homo sapi
c 231	19	2.4	138443	9	HS179E13	AL035603 Human DNA
c 232	19	2.4	138556	2	AC105564	AC105564 Rattus no
c 233	19	2.4	139566	2	AP004161	AP004161 Rattus sat
c 234	19	2.4	141775	2	AP004664	AP004664 Rattus sat
c 235	19	2.4	142021	2	AC092651	AC092651 Homo sapi
c 236	19	2.4	142629	2	AP002479	AP002479 Homo sapi
c 237	19	2.4	143438	2	AC094067	AC094067 Rattus no
c 238	19	2.4	143463	9	AL359312	AL359312 Human DNA
c 239	19	2.4	143542	2	AC108503	AC108503 Rattus no
c 240	19	2.4	143800	2	AC011875	AC011875 Homo sapi
c 241	19	2.4	144233	2	AC068103	AC068103 Homo sapi
c 242	19	2.4	144984	9	HSJ433F14	AL132766 Human DNA
c 243	19	2.4	146300	9	AL157903	AL157903 Human DNA
c 244	19	2.4	146619	2	OSJN00185	AL662980 Rattus sat
c 245	19	2.4	146950	2	AC095100	AC095100 Rattus no
c 246	19	2.4	147925	2	AC108182	AC108182 Felis cat
c 247	19	2.4	148338	2	AC079850	AC079850 Homo sapi
c 248	19	2.4	149870	9	AC024579	AC024579 Homo sapi
c 249	19	2.4	150401	2	AL139425	AL139425 Homo sapi
c 250	19	2.4	150651	9	AL357499	AL357499 Human DNA
c 251	19	2.4	151365	9	AC010382	AC010382 Homo sapi
c 252	19	2.4	151580	2	OSJN00049	AL606605 Rattus sat
c 253	19	2.4	151851	9	AC013731	AC013731 Homo sapi
c 254	19	2.4	152224	2	AC007933	AC007933 Homo sapi
c 255	19	2.4	152669	9	AL158087	AL158087 Human DNA
c 256	19	2.4	153234	2	AC026947	AC026947 Homo sapi
c 257	19	2.4	153929	2	AC011883	AC011883 Homo sapi
c 258	19	2.4	154384	2	AC015514	AC015514 Homo sapi
c 259	19	2.4	155519	2	AC083992	AC083992 Homo sapi
c 260	19	2.4	155907	2	AC105513	AC105513 Rattus no
c 261	19	2.4	156535	2	AC109344	AC109344 Homo sapi
c 262	19	2.4	157000	2	AC026511	AC026511 Homo sapi
c 263	19	2.4	157067	9	AC010163	AC010163 Homo sapi
c 264	19	2.4	157340	2	AC037493	AC037493 Homo sapi
c 265	19	2.4	157571	2	AC068255	AC068255 Homo sapi
c 266	19	2.4	157921	2	AC027726	AC027726 Homo sapi
c 267	19	2.4	158321	2	AC064810	AC064810 Homo sapi
c 268	19	2.4	158665	2	AC106526	AC106526 Rattus no
c 269	19	2.4	158744	2	AC094158	AC094158 Rattus no
c 270	19	2.4	160274	2	AC073411	AC073411 Homo sapi
c 271	19	2.4	160737	9	HS62F24	AL450003 Homo sapi
c 272	19	2.4	160815	2	AP001895	AP001895 Homo sapi
c 273	19	2.4	160952	9	AP003551	AP003551 Homo sapi
c 274	19	2.4	161207	2	AC092819	AC092819 Homo sapi
c 275	19	2.4	161900	9	AC096729	AC096729 Homo sapi
c 276	19	2.4	162150	9	AC093877	AC093877 Homo sapi
c 277	19	2.4	162828	2	AC106579	AC106579 Rattus no
c 278	19	2.4	163167	2	AC097407	AC097407 Rattus no
c 279	19	2.4	163246	2	AC068401	AC068401 Homo sapi
c 280	19	2.4	163347	2	AP001373	AP001373 Homo sapi
c 281	19	2.4	163372	2	AC087744	AC087744 Homo sapi
c 282	19	2.4	164198	2	AC016801	AC016801 Homo sapi
c 283	19	2.4	164285	2	AC025658	AC025658 Homo sapi
c 284	19	2.4	164820	9	AL627443	AL627443 Human DNA
c 285	19	2.4	165025	2	AC055871	AC055871 Homo sapi
c 286	19	2.4	165533	2	AC094484	AC094484 Rattus no
c 287	19	2.4	165616	9	AC073333	AC073333 Homo sapi
c 288	19	2.4	165655	2	AC027605	AC027605 Homo sapi
c 289	19	2.4	166451	9	AC018994	AC018994 Homo sapi
c 290	19	2.4	166585	9	AC078872	AC078872 Homo sapi
c 291	19	2.4	166894	9	CNS05TCQ	AL355836 Human chr
c 292	19	2.4	166941	2	AC073891	AC073891 Homo sapi
c 293	19	2.4	167348	2	AC013782	AC013782 Homo sapi
c 294	19	2.4	167521	30	AC067761	AC067761 Homo sapi
c 295	19	2.4	167564	2	AF267170	AF267170 Homo sapi
c 296	19	2.4	167919	2	AC090193	AC090193 Homo sapi
c 297	19	2.4	167966	2	AC015912	AC015912 Homo sapi
c 298	19	2.4	168285	9	AC008575	AC008575 Homo sapi
c 299	19	2.4	169078	2	AC094135	AC094135 Rattus no
c 300	19	2.4	169162	2	AC012479	AC012479 Homo sapi
c 301	19	2.4	169554	2	AC021379	AC021379 Homo sapi
c 302	19	2.4	170914	3	AC010843	AC010843 Drosophil
c 303	19	2.4	171225	2	AC024431	AC024431 Homo sapi
c 304	19	2.4	171241	2	AC021558	AC021558 Homo sapi
c 305	19	2.4	171368	9	HS095738	U95738 Human chrom
c 306	19	2.4	171390	9	AC027315	AC027315 Homo sapi
c 307	19	2.4	172024	2	AC078971	AC078971 Homo sapi
c 308	19	2.4	172694	2	CNS01DVS	AL136018 Homo sapi
c 309	19	2.4	172802	9	AC078817	AC078817 Homo sapi
c 310	19	2.4	172830	2	AP001320	AP001320 Homo sapi
c 311	19	2.4	173053	2	AC093523	AC093523 Homo sapi
c 312	19	2.4	173308	9	HS859D4	AL035668 Human DNA
c 313	19	2.4	173840	9	AC092445	AC092445 Homo sapi
c 314	19	2.4	173960	9	AC093885	AC093885 Homo sapi
c 315	19	2.4	173962	2	AC024155	AC024155 Homo sapi
c 316	19	2.4	174428	9	AC005821	AC005821 Homo sapi
c 317	19	2.4	174641	2	AC094401	AC094401 Rattus no
c 318	19	2.4	174994	2	AC025306	AC025306 Homo sapi
c 319	19	2.4	175368	9	CNS01DMF	AL137164 Human chr
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c 321	19	2.4	175574	2	AC084236	AC084236 Mus muscu
c 322	19	2.4	175602	2	AC097194	AC097194 Rattus no
c 323	19	2.4	177393	2	AC079019	AC079019 Homo sapi
c 324	19	2.4	177829	3	AC091127	AC091127 Drosophil
c 325	19	2.4	179289	2	AC024883	AC024883 Mus muscu
c 326	19	2.4	180317	2	AC025590	AC025590 Homo sapi
c 327	19	2.4	180489	2	AC090383	AC090383 Homo sapi
c 328	19	2.4	180590	9	AC106758	AC106758 Homo sapi
c 329	19	2.4	180919	9	AF088219	AF088219 Homo sapi
c 330	19	2.4	181179	9	AL161725	AL161725 Human DNA
c 331	19	2.4	181311	2	AC106862	AC106862 Homo sapi
c 332	19	2.4	181846	2	AC104651	AC104651 Homo sapi
c 333	19	2.4	181888	2	OSJN00129	AL607004 Rattus sat
c 334	19	2.4	181926	2	AC008461	AC008461 Homo sapi
c 335	19	2.4	181911	9	AC025882	AC025882 Homo sapi
c 336	19	2.4	182175	2	AC013362	AC013362 Homo sapi
c 337	19	2.4	182643	2	AP002794	AP002794 Homo sapi
c 338	19	2.4	182948	2	AL671910	AL671910 Mus muscu
c 339	19	2.4	183205	2	AC013638	AC013638 Homo sapi
c 340	19	2.4	183290	2	AC012569	AC012569 Homo sapi
c 341	19	2.4	183461	9	AC006121	AC006121 Homo sapi
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c 344	19	2.4	184244	2	AC073282	AC073282 Homo sapi
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c 346	19	2.4	184906	2	CNS07ECY	AL445363 Homo sapi
c 347	19	2.4	185573	2	AC010994	AC010994 Drosophil
c 348	19	2.4	185679	2	AL611935	AL611935 Mus muscu
c 349	19	2.4	185967	9	CNS01DVR	AL136001 Human chr
c 350	19	2.4	185981	2	AC095185	AC095185 Rattus no
c 351	19	2.4	186464	9	AC092839	AC092839 Homo sapi
c 352	19	2.4	186709	2	AC091192	AC091192 Homo sapi
c 353	19	2.4	186962	9	AP000848	AP000848 Homo sapi
c 354	19	2.4	187617	2	AC084082	AC084082 Homo sapi
c 355	19	2.4	187691	10	AC083816	AC083816 Mus muscu
c 356	19	2.4	188107	9	CNS01DWE	AL137129 Human chr
c 357	19	2.4	189371	2	AC023125	AC023125 Homo sapi
c 358	19	2.4	189897	2	AC104829	AC104829 Homo sapi
c 359	19	2.4	190672	2	AC105890	AC105890 Rattus no
c 360	19	2.4	190843	8	AP002863	AP002863 Rattus sat
c 361	19	2.4	190875	2	AC022255	AC022255 Homo sapi
c 362	19	2.4	191360	2	AL663079	AL663079 Mus muscu
c 363	19	2.4	191770	2	AC093616	AC093616 Homo sapi
c 364	19	2.4	191835	2	AC007595	AC007595 Homo sapi
c 365	19	2.4	192083	2	AC015901	AC015901 Homo sapi

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C 366	19	2.4 192393	3	AC0100332
C 367	19	2.4 192867	9	AL358815
C 368	19	2.4 192952	2	AC026966
C 369	19	2.4 193116	2	AF003847
C 371	19	2.4 193526	3	AC010993
C 372	19	2.4 193645	2	AC015953
C 373	19	2.4 194032	2	AC019151
C 374	19	2.4 194101	2	AC019151
C 375	19	2.4 195079	2	AC090910
C 376	19	2.4 195799	2	AC104600
C 377	19	2.4 196054	2	AC087742
C 378	19	2.4 196392	2	AC011474
C 379	19	2.4 196606	2	AC087292
C 380	19	2.4 197152	9	AF000779
C 381	19	2.4 197310	2	AC108145
C 382	19	2.4 197663	9	AF254981
C 383	19	2.4 197817	2	AC009245
C 384	19	2.4 198501	2	AP001185
C 385	19	2.4 199365	2	AC108054
C 386	19	2.4 199554	30	AC068485
C 387	19	2.4 200767	2	AC009552
C 388	19	2.4 200889	2	AC009652
C 389	19	2.4 200976	2	AC024191
C 390	19	2.4 202423	2	AC100753
C 391	19	2.4 203043	9	AL604025
C 392	19	2.4 203278	9	AC017093
C 393	19	2.4 204168	10	AC010482
C 394	19	2.4 204654	9	AF146793
C 395	19	2.4 205638	2	CNS057C9
C 396	19	2.4 206235	2	AC040927
C 397	19	2.4 206819	2	AC107486
C 398	19	2.4 208813	9	AC016029
C 399	19	2.4 208925	2	AC090467
C 400	19	2.4 209066	2	AC092425
C 401	19	2.4 209221	2	AL603856
C 402	19	2.4 209221	2	AC080058
C 403	19	2.4 210146	2	AC080038
C 404	19	2.4 210176	2	AC068528
C 405	19	2.4 210837	2	AC016432
C 406	19	2.4 212713	2	AC016885
C 407	19	2.4 212865	2	AC091318
C 408	19	2.4 214967	2	AC092207
C 409	19	2.4 215004	9	AC093166
C 410	19	2.4 215196	2	AC085507
C 411	19	2.4 215936	9	AL603705
C 412	19	2.4 216920	2	CNS057CA
C 413	19	2.4 216995	2	AL583892
C 414	19	2.4 220995	2	AC010687
C 415	19	2.4 223136	2	AC095297
C 416	19	2.4 223725	2	AC005820
C 417	19	2.4 224029	2	AC008636
C 418	19	2.4 224712	2	AL606963
C 419	19	2.4 228497	2	AL606963
C 420	19	2.4 233830	2	AC107464
C 421	19	2.4 234057	2	AC071731
C 422	19	2.4 240995	2	AC095993
C 423	19	2.4 241280	2	AC027766
C 424	19	2.4 245327	2	AC020854
C 425	19	2.4 257702	2	AL662891
C 426	19	2.4 269711	3	CEY111B2A
C 427	19	2.4 279913	2	AP000408
C 428	19	2.4 298839	3	AC096952
C 429	19	2.4 300728	2	AC003492
C 430	19	2.4 301450	1	AC095925
C 431	19	2.4 301711	1	AP003185
C 432	19	2.4 307962	1	AP002564
C 433	19	2.4 335913	6	AX196295
C 434	18	2.3 108 5	5	AX196295
C 435	18	2.3 180 5	5	AF049955
C 436	18	2.3 180 9	9	HS75B3R
C 437	18	2.3 200 11	11	G21681
C 438	18	2.3 246 9	9	AF086001
		263 9		262906 H
				262907 H

c 512	18	2.3	5031	10	AF199332	AF199332 Rattus no	c 585	18	2.3	44583	9	AC000083	AC000083 Homo sapi
c 513	18	2.3	5079	10	AF199325	AF199325 Rattus no	c 586	18	2.3	45255	2	AC101034	AC101034 Mus muscu
c 514	18	2.3	5133	9	HSFLA1A	Y00796 Human mRNA	c 587	18	2.3	45291	2	AC093987	AC093987 Rattus no
c 515	18	2.3	5172	10	AF199324	AF199324 Rattus no	c 588	18	2.3	47507	2	AC017676	AC017676 Drosophil
c 516	18	2.3	5223	6	AX252154	AX252154 Sequence	c 589	18	2.3	47724	8	AC007119	AC007119 Arabidops
c 517	18	2.3	5233	6	AX344520	AX344520 Sequence	c 590	18	2.3	50785	8	AC007169	AC007169 Arabidops
c 518	18	2.3	5233	6	AX348927	AX348927 Sequence	c 591	18	2.3	54526	2	AC087404	AC087404 Homo sapi
c 519	18	2.3	5253	6	AX349897	AX349897 Sequence	c 592	18	2.3	58423	2	AC087660	AC087660 Homo sapi
c 520	18	2.3	5550	10	AF199331	AF199331 Rattus no	c 593	18	2.3	59026	2	AC101623	AC101623 Mus muscu
c 521	18	2.3	5592	10	AF199330	AF199330 Rattus no	c 594	18	2.3	60318	2	AC110240	AC110240 Mus muscu
c 522	18	2.3	5640	10	AF199332	AF199332 Rattus no	c 595	18	2.3	60610	9	AL591470	AL591470 Human DNA
c 523	18	2.3	5680	6	AX346731	AX346731 Sequence	c 596	18	2.3	61169	9	AP001433	AP001433 Homo sapi
c 524	18	2.3	5788	8	ALPAAAT2A	L25435 Medicago sa	c 597	18	2.3	61623	2	AC108413	AC108413 Mus muscu
c 525	18	2.3	6012	6	AX251974	AX251974 Sequence	c 598	18	2.3	61823	2	AC108413	AC108413 Human DNA
c 526	18	2.3	6012	6	AX344366	AX344366 Sequence	c 599	18	2.3	62493	9	HS193615	HS193615 Human DNA
c 527	18	2.3	6012	6	AX348759	AX348759 Sequence	c 600	18	2.3	62612	2	AC107699	AC107699 Mus muscu
c 528	18	2.3	6113	9	F325326S06	AF325331 Homo sapi	c 601	18	2.3	62856	2	AC108314	AC108314 Rattus no
c 529	18	2.3	6606	8	FN062895	U62895 Emericella	c 602	18	2.3	63212	2	AC107153	AC107153 Drosophil
c 530	18	2.3	6962	8	AB000125	AB000125 Aspergill	c 603	18	2.3	63212	2	AC110252	AC110252 Mus muscu
c 531	18	2.3	7226	14	S74099	S74099 Avian myelo	c 604	18	2.3	63767	8	ATAC023912	ATAC023912 Arabidops
c 532	18	2.3	7692	10	AB030013	AB030013 Mus muscu	c 605	18	2.3	64582	8	AC027037	AC027037 Oryza sat
c 533	18	2.3	8064	6	AX346288	AX346288 Sequence	c 606	18	2.3	65493	2	AC099807	AC099807 Homo sapi
c 534	18	2.3	9646	6	AX346591	AX346591 Sequence	c 607	18	2.3	65493	2	AC099807	AC099807 Homo sapi
c 535	18	2.3	10820	6	AX305711	AX305711 Sequence	c 608	18	2.3	66008	9	AC023190	AC023190 Homo sapi
c 536	18	2.3	10820	10	MMU062021	U62021 Mus musculu	c 609	18	2.3	66375	2	AC100703	AC100703 Mus muscu
c 537	18	2.3	10951	1	AE007263	AE007263 Sinorhizo	c 610	18	2.3	66714	2	AC110187	AC110187 Mus muscu
c 538	18	2.3	11015	6	AX280003	AX280003 Sequence	c 611	18	2.3	66966	2	AC026842	AC026842 Homo sapi
c 539	18	2.3	11015	6	AX281190	AX281190 Sequence	c 612	18	2.3	67780	2	AC087275	AC087275 Homo sapi
c 540	18	2.3	11015	6	AX336459	AX336459 Sequence	c 613	18	2.3	68003	2	AC090851	AC090851 Homo sapi
c 541	18	2.3	11262	1	AE004170	AE004170 Vibrio ch	c 614	18	2.3	68723	2	AC019515	AC019515 Drosophil
c 542	18	2.3	11557	9	AF187881	AF187881 Homo sapi	c 615	18	2.3	68991	2	AC102157	AC102157 Mus muscu
c 543	18	2.3	11726	6	AX346964	AX346964 Sequence	c 616	18	2.3	69451	2	AC080049	AC080049 Homo sapi
c 544	18	2.3	12054	6	AX346080	AX346080 Sequence	c 617	18	2.3	69471	2	AL596452	AL596452 Human DNA
c 545	18	2.3	12307	2	AC024562_4	Continuation (5 of	c 618	18	2.3	69682	9	AP001300	AP001300 Arabidops
c 546	18	2.3	12537	6	AR069468	AR069468 Sequence	c 619	18	2.3	71327	8	AP001300	AP001300 Arabidops
c 547	18	2.3	12537	6	AR162785	AR162785 Sequence	c 620	18	2.3	72173	2	AC105149	AC105149 Rattus no
c 548	18	2.3	12599	3	AC024743	AC024743 Caenorhab	c 621	18	2.3	72596	2	AC025598	AC025598 Mus muscu
c 549	18	2.3	13131	6	AX356424	AX356424 Sequence	c 622	18	2.3	74962	6	AB019230	AB019230 Arabidops
c 550	18	2.3	14543	1	AE001691	AE001691 Thermotog	c 623	18	2.3	75611	2	AC102539	AC102539 Mus muscu
c 551	18	2.3	15218	2	AC014602	AC014602 Drosophil	c 624	18	2.3	75611	2	AL354983	AL354983 Human DNA
c 552	18	2.3	15755	10	MMU20949	U20949 Mus musculu	c 625	18	2.3	77331	9	AL354983	AL354983 Human DNA
c 553	18	2.3	16157	2	AC012931	AC012931 Drosophil	c 626	18	2.3	77331	9	AB010077	AB010077 Arabidops
c 554	18	2.3	17343	2	AC104491	AC104491 Trypanoso	c 627	18	2.3	77380	8	AB010077	AB010077 Arabidops
c 555	18	2.3	17421	6	AX277891	AX277891 Sequence	c 628	18	2.3	78184	9	AC067722	AC067722 Homo sapi
c 556	18	2.3	17421	6	AX233568	AX233568 Sequence	c 629	18	2.3	78485	2	AC027593	AC027593 Homo sapi
c 557	18	2.3	17421	6	AX233568	AX233568 Sequence	c 630	18	2.3	79414	2	AC023502	AC023502 Homo sapi
c 558	18	2.3	17720	2	AC104495	AC104495 Trypanoso	c 631	18	2.3	79509	9	AL353769	AL353769 Human DNA
c 559	18	2.3	17986	3	CEL2K75	U23451 Caenorhabdi	c 632	18	2.3	79531	9	AL390037	AL390037 Human DNA
c 560	18	2.3	20029	9	AL589646	AL589646 Human DNA	c 633	18	2.3	80376	3	AC004442	AC004442 Drosophil
c 561	18	2.3	20587	9	HS185E6A	Z68274 Human DNA S	c 634	18	2.3	80376	2	AC095072	AC095072 Rattus no
c 562	18	2.3	20598	6	AX067857	AX067857 Sequence	c 635	18	2.3	80710	2	AB026645	AB026645 Arabidops
c 563	18	2.3	20872	9	AP000222	AP000222 Homo sapi	c 636	18	2.3	81020	8	AB026645	AB026645 Arabidops
c 564	18	2.3	22586	3	AC094018	AC094018 Trypanoso	c 637	18	2.3	81347	8	AB015478	AB015478 Arabidops
c 565	18	2.3	22843	2	AC015232	AC015232 Drosophil	c 638	18	2.3	82912	3	AC004574	AC004574 Drosophil
c 566	18	2.3	25659	10	AB022160	AB022160 Mus muscu	c 639	18	2.3	82912	9	AL135928	AL135928 Human DNA
c 567	18	2.3	25659	10	AB023029	AB023029 Arabidops	c 640	18	2.3	83253	8	AP000383	AP000383 Arabidops
c 568	18	2.3	29663	2	AC014990	AC014990 Drosophil	c 641	18	2.3	83389	8	AL603713	AL603713 Human DNA
c 569	18	2.3	30616	2	AC018027	AC018027 Drosophil	c 642	18	2.3	84203	8	AC005106	AC005106 Genomic s
c 570	18	2.3	31209	8	SPCC18B5	AL109736 S.pombe c	c 643	18	2.3	84497	10	AC091421	AC091421 Mus muscu
c 571	18	2.3	31999	8	AC092777	AC092777 Leishmani	c 644	18	2.3	85918	2	DMB934H2	DMB934H2 Drosophil
c 572	18	2.3	32000	2	AC045638	AC045638 Caenorhab	c 645	18	2.3	85992	8	ATF2G14	ATF2G14 Arabidops
c 573	18	2.3	33772	3	AF045638	AF045638 Caenorhab	c 646	18	2.3	86554	8	AB005245	AB005245 Arabidops
c 574	18	2.3	34561	2	AC015420	AC015420 Drosophil	c 647	18	2.3	86630	9	AB005245	AB005245 Arabidops
c 575	18	2.3	35469	8	HS786D3	AL023801 Human DNA	c 648	18	2.3	86973	8	AC079402	AC079402 Homo sapi
c 576	18	2.3	35930	8	AC079288	AC079288 Arabidops	c 649	18	2.3	87244	2	AC097775	AC097775 Rattus no
c 577	18	2.3	38614	2	AC107503	AC107503 Rattus no	c 650	18	2.3	87420	2	AC095766	AC095766 Rattus no
c 578	18	2.3	38865	2	AC019934	AC019934 Drosophil	c 651	18	2.3	88380	2	CNS05TDL	CNS05TDL Homo sapi
c 579	18	2.3	39006	3	AF077531	AF077531 Caenorhab	c 652	18	2.3	88484	9	AL355794	AL355794 Human DNA
c 580	18	2.3	40018	9	HS10111	AL109616 Homo sapi	c 653	18	2.3	88816	2	AC097900	AC097900 Rattus no
c 581	18	2.3	40331	9	AL590223	AL590223 Human DNA	c 654	18	2.3	88871	10	MMU58105	MMU58105 Mus musculu
c 582	18	2.3	41015	9	HS590K14	AL049198 Human DNA	c 655	18	2.3	89487	9	AL138808	AL138808 Human DNA
c 583	18	2.3	41052	9	AC002499	AC002499 Human Cos	c 656	18	2.3	89669	9	AL109755	AL109755 Human DNA
c 584	18	2.3	41609	3	CELCO3A7	AF016451 Caenorhab	c 657	18	2.3	91340	9	AC008898	AC008898 Homo sapi
	18	2.3	44571	2	AC104968	AC104968 Homo sapi		18	2.3	92118	9	AC074384	AC074384 Homo sapi

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c 658	18	2.3	92458	9	AL353715	Human DNA	c 731	18	2.3	123369	9	AC025170	Homo sapi
c 659	18	2.3	92705	9	AC006327	Homo sapi	c 732	18	2.3	123489	9	HSBA27F12	Human DNA
c 660	18	2.3	92741	8	AP004473	Lotus jap	c 733	18	2.3	123805	9	AC002464	Human BAC
c 661	18	2.3	92918	2	AC020050	Drosophila	c 734	18	2.3	124025	9	AL160169	Human DNA
c 662	18	2.3	93244	2	AC090062	Homo sapi	c 735	18	2.3	124885	2	AC087346	Homo sapi
c 663	18	2.3	93708	9	AL135934	Human DNA	c 736	18	2.3	124927	2	AC010475	Homo sapi
c 664	18	2.3	93764	2	AC074072	Homo sapi	c 737	18	2.3	125439	9	AC010485	Human DNA
c 665	18	2.3	93795	2	AC015381	Drosophila	c 738	18	2.3	125500	9	HS1018K9	Homo sapi
c 666	18	2.3	94891	9	AC022428	Homo sapi	c 739	18	2.3	125746	9	AC010589	Homo sapi
c 667	18	2.3	95481	9	AC024192	Homo sapi	c 740	18	2.3	125933	9	AC003510	Homo sapi
c 668	18	2.3	95554	2	AC093284	Homo sapi	c 741	18	2.3	126327	9	AC005252	Homo sapi
c 669	18	2.3	96654	9	AC004783	Homo sapi	c 742	18	2.3	126382	2	AC008879	Human DNA
c 670	18	2.3	96899	8	AC001328	Arabidops	c 743	18	2.3	126825	2	HS11077B9	Human DNA
c 671	18	2.3	98002	9	AL353147	Human DNA	c 744	18	2.3	126923	2	AC095554	Rattus no
c 672	18	2.3	98195	2	AC098045	Rattus no	c 745	18	2.3	127425	9	AC004976	Homo sapi
c 673	18	2.3	98595	9	AP001329	Homo sapi	c 746	18	2.3	127834	9	AC003958	Homo sapi
c 674	18	2.3	98589	2	AC107563	Rattus no	c 747	18	2.3	128220	9	AC004457	Homo sapi
c 675	18	2.3	99589	2	AC093299	Homo sapi	c 748	18	2.3	128473	9	AC004241	Homo sapi
c 676	18	2.3	99637	2	AC096802	Rattus no	c 749	18	2.3	128710	9	HSJ119H20	Human DNA
c 677	18	2.3	99923	8	F508	Arabidops	c 750	18	2.3	129838	8	AC004241	Homo sapi
c 678	18	2.3	100000	9	AB020864	Homo sapi	c 751	18	2.3	129922	9	AC004241	Homo sapi
c 679	18	2.3	100000	9	AP000085	Homo sapi	c 752	18	2.3	130278	9	AC007903	Homo sapi
c 680	18	2.3	100000	9	AP000137	Homo sapi	c 753	18	2.3	130414	2	AC005664	Homo sapi
c 681	18	2.3	100000	9	AP000158	Homo sapi	c 754	18	2.3	130583	2	AC007737	Rattus no
c 682	18	2.3	100000	8	ATF181L15	Arabidops	c 755	18	2.3	130653	8	AC068667	Arabidops
c 683	18	2.3	100328	8	AL133298	Arabidops	c 756	18	2.3	131081	2	AF165145	Homo sapi
c 684	18	2.3	100786	2	AC013972	Drosophila	c 757	18	2.3	131274	9	AC069506	Homo sapi
c 685	18	2.3	101027	9	AC023160	Homo sapi	c 758	18	2.3	131473	8	AC005171	Homo sapi
c 686	18	2.3	101121	2	AC097166	Rattus no	c 759	18	2.3	131727	9	AC093850	Homo sapi
c 687	18	2.3	101453	2	AC098252	Rattus no	c 760	18	2.3	131872	2	AC105528	Homo sapi
c 688	18	2.3	101670	2	AL590005	Human DNA	c 761	18	2.3	132244	2	AC093178	Rattus no
c 689	18	2.3	101966	8	AC105714	Rattus no	c 762	18	2.3	132614	10	AC021756	Mus muscu
c 690	18	2.3	102183	9	AC027134	Arabidops	c 763	18	2.3	133780	2	AL356293	Homo sapi
c 691	18	2.3	102892	9	AL359813	Human DNA	c 764	18	2.3	134371	3	AC008143	Drosophila
c 692	18	2.3	102994	2	AC099083	Human DNA	c 765	18	2.3	134550	9	HS217522	Human DNA
c 693	18	2.3	103157	8	AC011810	Arabidops	c 766	18	2.3	134687	9	AL445259	Human DNA
c 694	18	2.3	103567	8	YUP8H12	Arabidops	c 767	18	2.3	134995	9	AL160398	Human DNA
c 695	18	2.3	104436	6	HS611N7	Rattus no	c 768	18	2.3	135631	9	AL512849	Human DNA
c 696	18	2.3	105956	2	AC098919	Rattus no	c 769	18	2.3	136294	2	AC092781	Oryza sat
c 697	18	2.3	107139	2	AL360223	Homo sapi	c 770	18	2.3	136497	2	AC099677	Homo sapi
c 698	18	2.3	109389	9	AC002530	Human DNA	c 771	18	2.3	136540	10	AL606487	Mouse DNA
c 699	18	2.3	109612	9	AL512503	Human DNA	c 772	18	2.3	136952	2	AC018487	Drosophila
c 700	18	2.3	109813	9	HSJ180E22	Human DNA	c 773	18	2.3	137137	9	AC004928	Homo sapi
c 701	18	2.3	110000	2	AC073604	Continuation (3 of	c 774	18	2.3	137243	2	AP003894	Oryza sat
c 702	18	2.3	110000	2	AC092202	Continuation (2 of	c 775	18	2.3	137391	9	AL161732	Human DNA
c 703	18	2.3	110000	2	AC026388	Continuation (2 of	c 776	18	2.3	137848	9	AL136368	Human DNA
c 704	18	2.3	110338	3	AC006066	Rattus no	c 777	18	2.3	138033	2	AC093265	Homo sapi
c 705	18	2.3	111122	2	AC094837	Rattus no	c 778	18	2.3	138036	2	AP004762	Oryza sat
c 706	18	2.3	111122	2	AC066604	Homo sapi	c 779	18	2.3	138490	10	MMU249895	Mus muscu
c 707	18	2.3	112298	9	AC068370	Homo sapi	c 780	18	2.3	138936	2	AP004563	Oryza sat
c 708	18	2.3	112390	9	AC016607	Homo sapi	c 781	18	2.3	139121	2	AL135916	Homo sapi
c 709	18	2.3	112535	2	AC103152	Rattus no	c 782	18	2.3	139134	2	AL135916	Homo sapi
c 710	18	2.3	113367	2	AC008178	Homo sapi	c 783	18	2.3	139434	2	AP004754	Oryza sat
c 711	18	2.3	113501	2	AC011398	Homo sapi	c 784	18	2.3	139518	2	AC103044	Rattus no
c 712	18	2.3	114008	2	AC093780	Homo sapi	c 785	18	2.3	140098	2	AC024510	Homo sapi
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c 715	18	2.3	115468	2	AC011820	Homo sapi	c 788	18	2.3	141892	2	AC023197	Homo sapi
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c 719	18	2.3	116824	9	AC010245	Homo sapi	c 792	18	2.3	142636	2	AC104122	Homo sapi
c 720	18	2.3	117840	9	HSJ442L6	Human DNA	c 793	18	2.3	142986	2	AC023467	Homo sapi
c 721	18	2.3	118524	9	AL157878	Human DNA	c 794	18	2.3	143057	2	AL591515	Homo sapi
c 722	18	2.3	118873	9	AL157878	Human DNA	c 795	18	2.3	143422	30	AC011972	Homo sapi
c 723	18	2.3	118955	2	AC068274	Homo sapi	c 796	18	2.3	143642	9	AC097715	Homo sapi
c 724	18	2.3	120192	2	AC093220	Homo sapi	c 797	18	2.3	143967	9	AC097715	Homo sapi
c 725	18	2.3	120219	9	AL355540	Human DNA	c 798	18	2.3	144070	2	AC027566	Homo sapi
c 726	18	2.3	120955	9	HUAC002310	Human Chr	c 799	18	2.3	144075	9	AL353139	Homo sapi
c 727	18	2.3	121598	9	AC006012	Homo sapi	c 800	18	2.3	144156	9	AL160276	Human DNA
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c 807	18	2.3 147431	2	AC020996	Homo sapi	880	18	2.3 159362	9	AL589741	Human DNA
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c 827	18	2.3 152366	9	AL138894	Human DNA	900	18	2.3 163179	9	AC013549	Homo sapi
c 828	18	2.3 152443	3	AC009208	Drosophila	c 901	18	2.3 163301	9	CNS01DMB	Rattus no
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c 831	18	2.3 152685	9	AC008818	Homo sapi	c 904	18	2.3 163577	9	AL590428	Human DNA
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c 841	18	2.3 154018	2	AC062019	Homo sapi	c 914	18	2.3 164794	2	AC087361	Homo sapi
c 842	18	2.3 154158	2	AL365257	Homo sapi	c 915	18	2.3 164839	8	AP002844	Oryza sat
c 843	18	2.3 154242	2	AL442071	Homo sapi	c 916	18	2.3 164863	2	AC026517	Homo sapi
c 844	18	2.3 154618	2	AC073403	Homo sapi	917	18	2.3 164991	9	AC011088	Homo sapi
c 845	18	2.3 154706	2	AC008470	Homo sapi	918	18	2.3 165016	9	AC024559	Homo sapi
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c 847	18	2.3 155359	9	AP003689	Homo sapi	c 920	18	2.3 165082	2	AC106856	Homo sapi
c 848	18	2.3 155376	2	AC027026	Homo sapi	921	18	2.3 165118	3	AC108488	Drosophila
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ALIGNMENTS

RESULT 1
AX063181
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AX063181
Sequence 808 from Patent WO0100828.
AX063181
AX063181.1 GI:12541027
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 781)
Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S.,
Carter,D., Retter,M.W. and Mannion,J.
Compositions and methods for the therapy and diagnosis of lung
cancer
Patent: WO 0100828-A 808 04-JAN-2001;

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Sequence 808 from Patent WO0100828.
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AX063181.1 GI:12541027
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Homo sapiens
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1 (bases 1 to 781)
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Compositions and methods for the therapy and diagnosis of lung
cancer
Patent: WO 0100828-A 808 04-JAN-2001;

FEATURES	CORIXA CORPORATION (US)	Location/Qualifiers	Score 781; DB 6; Length 781;	Indels 0; Gaps 0;
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RESULT 2				
LOCUS	HS318878			
DEFINITION	Homo sapiens mRNA for XAGE-1c protein.	740 bp	mRNA	linear
	HS318878			PRI 14-JAN-2002

ACCESSION AJ318878
VERSION AJ318878.1 GI:18157205
KEYWORDS XAGE-1c gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Zendman,A.J.W., van Kraats,A., Weidle,U.H., Ruiter,D.R. and Van
Muijen,G.N.P.
TITLE Expression profile of members of the XAGE cancer/testis antigen
family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 740)
AUTHORS Zendman,A.J.W.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-2001) Zendman A.J.W., Department of Pathology,
University Medical Center St Radboud, Geert Grooteplein Zuid 24, PO
Box 9101 6500 HB Nijmegen, NETHERLANDS
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Qy 100 AGTTGAAGTGTGAGTGAAGAGGACACAGCAGGCTTCCGGAGGGTTGTCTGTGCTCA 159
Db 61 AGTTGAAGTGTGAGTGAAGAGGACACAGCAGGCTTCCGGAGGGTTGTCTGTGCTCA 120
Qy 160 GTGACTCAGAGTGAGAGGCCCTCGAAGTCGTCTGTCCTCTCATGCGGTGCCACGCCAT 219
Db 121 GTGACTCAGAGTGAGAGGCCCTCGAAGTCGTCTGTCCTCTCATGCGGTGCCACGCCAT 180
Qy 220 GGACCTCTTCTCGTCACGGCCATAACTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 279
Db 181 GGACCTCTTCTCGTCACGGCCATAACTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
Qy 280 GCTCAGGCGAAGCTGGGGTCTGTGTGGGGTATCCGAGTCCCAGAGCACCTGGAAACCCC 339
Db 241 GCTCAGGCGAAGCTGGGGTCTGTGTGGGGTATCCGAGTCCCAGAGCACCTGGAAACCCC 300
Qy 340 GACAGAGATTCTGGACTCCCGACACGGGACCGAGGAGGAGGAGGAGGAGGAGGAGGAG 399
Db 301 GACAGAGATTCTGGACTCCCGACACGGGACCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Qy 400 CAACACAGAACACACAGCCAGTCCCGAGGAGGCCAGTAAATGGAGAGCCCAAAAGAG 459
Db 361 CAACACAGAACACACAGCCAGTCCCGAGGAGGCCAGTAAATGGAGAGCCCAAAAGAG 420

Qy 460 AACGAGCAGCTGAAAGTCGGGATCCTACACCTGGCGAGCAGACAGAAAGATCAGGATA 519
Db 421 AACGAGCAGCTGAAAGTCGGGATCCTACACCTGGCGAGCAGACAGAAAGATCAGGATA 480
Qy 520 CAGCTGAGATCCCAGTGCAGGACATGGAAGTGATCTGCAAGAGCTGCATCAGTCAACA 579
Db 481 CAGCTGAGATCCCAGTGCAGGACATGGAAGTGATCTGCAAGAGCTGCATCAGTCAACA 540
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Qy 640 CACTGTAAAAATGCCAGAACGAGTGAAGAGCAACCAACCAAGTTTAAATGAAGACAAGCTGA 699
Db 601 CACTGTAAAAATGCCAGAACGAGTGAAGAGCAACCAACCAAGTTTAAATGAAGACAAGCTGA 660
Qy 700 AACACGCAAGCTGGTTTATATATAGATATTTGACTTAACTATCTCAATAAAGTTTGC 759
Db 661 AACACGCAAGCTGGTTTATATATAGATATTTGACTTAACTATCTCAATAAAGTTTGC 720
Qy 760 AGCTTTTCAACCAAAAAA 779
Db 721 AGCTTTTCAACCAAAAAA 740
RESULT 3
LOCUS BC009538 529 bp mRNA linear PRI 22-OCT-2001
DEFINITION Homo sapiens, clone MGC:10063 IMAGE:3893227, mRNA, complete cds.
ACCESSION BC009538
VERSION BC009538.1 GI:16306934
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 529)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (29-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAX Plate: 14 Row: g Column: 8.
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Query Match      67.3%; Score 526; DB 9; Length 529;
Best Local Similarity 100.0%; Pred. No. 5.3e-233; Indels 0; Gaps 0;
Matches 526; Conservative 0; Mismatches 0;
Qy 256 GAAGGAGGGCCGAGGAGTGGAGGGCTCAGCGGAAGCTGGGTGCTGTGGGGCTATPCG 315
Db 1 GAAGGAGGGCCGAGGAGTGGAGGGCTCAGCGGAAGCTGGGTGCTGTGGGGCTATPCG 60
Qy 316 AGTCCCAGAAGCACTGGGAACCCCGACAGAAAGATTCTGGACATCCCGACAGCGGAGCAGGA 375
Db 61 AGTCCCAGAAGCACTGGGAACCCCGACAGAAAGATTCTGGACATCCCGACAGCGGAGCAGGA 120
Qy 376 GAGGAGCGGATGAGCGACACACACAACACACAGCAAGCCAGTCCCGACAGCAACCA 435
Db 121 GAGGAGCGGATGAGCGACACACACAACACACAGCAAGCCAGTCCCGACAGCAACCA 180
Qy 436 GTAATGAGAGCCCCAAAAGAGAACACAGCACTGAAAGTGGGATGCTTACACCTGGGC 495
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Qy 496 AGCAGACAGAGAGATCAGGATACAGCTCAGATCCAGTCCGCGACATGGAAGGTGATC 555
Db 241 AGCAGACAGAGAGATCAGGATACAGCTCAGATCCAGTCCGCGACATGGAAGGTGATC 300
Qy 556 TCGAAGAGCTGCATCAGTCAACACCCGGGATAAATCTGGATTTGGTTCCGCGCTCAAG 615
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Qy 616 GTGAAGATAATACCTAAGAGGACACTGTAAATGCCAGACAGGTCAAGAGCAACCA 675
Db 361 GTGAAGATAATACCTAAGAGGACACTGTAAATGCCAGACAGGTCAAGAGCAACCA 420
Qy 676 CAAGTTTAAATGAGACAAAGCTGAAACACCGCAAGCTGGTTTTATATTAGATATTGACT 735
Db 421 CAAGTTTAAATGAGACAAAGCTGAAACACCGCAAGCTGGTTTTATATTAGATATTGACT 480
Qy 736 TAAACTATCTCAATAAGATTTTCCAGCTTTCACCAAAAAA 781
Db 481 TAAACTATCTCAATAAGATTTTCCAGCTTTCACCAAAAAA 526

RESULT 4
HSA400997      6060 bp      DNA      linear      PRI 05-MAY-2001
LOCUS
DEFINITION      Homo sapiens XAGE-1b gene for cancer/testis-associated protein
XAGE-1b, exons 1-4.
ACCESSION      AJ400997
VERSION      AJ400997.1 GI:13992557
KEYWORDS      cancer/testis-associated protein; XAGE-1b gene.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 6060)
Zendman,A.J.W., van Kraals,A.A., Weidie,U.H., Ruiter,D.J. and Van
Muijen,G.N.P.
XAGE-1b, a novel cancer/testis-associated gene, induced in melanoma
metastases
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 6060)
AUTHORS      Zendman,A.J.W.
TITLE      Direct Submission
JOURNAL      Submitted (24-MAY-2000) Zendman A.J.W., Pathology, University
Medical Center St. Radboud, Geert Grooteplein Zuid 24, Nijmegen,
6500 HB POBox 9101, NETHERLANDS
FEATURES      Location/Qualifiers
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BASE COUNT      1700 a      1184 c      1420 g      1756 t
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Query Match      50.2%; Score 392; DB 9; Length 6060;
Best Local Similarity 100.0%; Pred. No. 3.6e-171;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGGCGGAGCTGTGAGCGGGGACTCGGCTCCTGAGGTCTGGATTCTTTCTCCGCTACT 60
Db 665 GCGGCGGAGCTGTGAGCGGGGACTCGGCTCCTGAGGTCTGGATTCTTTCTCCGCTACT 724
Qy 61 GAGACACGGCGGTAGGTCCACAGGCAGATCCAAATGGGAGTTGAAGTGTGAGTGAGACT 120
Db 725 GAGACACGGCGGTAGGTCCACAGGCAGATCCAAATGGGAGTTGAAGTGTGAGTGAGACT 784
Qy 121 GAAGAGAACCCAGCAGGCTTCGGAGGGTGTCTGTGCTGACTCAGACTCAGAGTGAGAGGCC 180
Db 785 GAAGAGAACCCAGCAGGCTTCGGAGGGTGTGTGTGCTGACTCAGACTCAGAGTGAGAGGCC 844
Qy 181 CTCGAAGTGTGTCTCTCTCATGCGGTGCCAGCCCATGGACCTTCTTGTCTCGTCAAG 240
Db 845 CTCGAAGTGTGTCTCTCTCATGCGGTGCCAGCCCATGGACCTTCTTGTCTCGTCAAG 904
Qy 241 GCCATAACTAGGAGGAAGGGCCGAGAGTGGAGGGCTCAGGCCGAAGCTGGGGTGC 300
Db 905 GCCATAACTAGGAGGAAGGGCCGAGAGTGGAGGGCTCAGGCCGAAGCTGGGGTGC 964
Qy 301 TGTGGGGGTATCCGAGTCCCAGAAGCACTGGAACCCCGACAGAGATTTCTGGACTCCC 360
Db 965 TGTGGGGGTATCCGAGTCCCAGAAGCACTGGAACCCCGACAGAGATTTCTGGACTCCC 1024
Qy 361 CAGACCGGACCCAGGAGGAGCGGATGACG 392
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Db	1025	CAGACGGACGAGGACCGCATGACG	1056	
RESULT 5				
AC025553/c				
LOCUS				
DEFINITION	AC025553	180859 bp	DNA	linear HTG 01-SEP-2000
	Homo sapiens chromosome X clone RP11-485B17, WORKING DRAFT			
	SEQUENCE, 23 unordered pieces.			
ACCESSION	AC025553			
VERSION	AC02553.5	GI:9958270		
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.			
SOURCE				
ORGANISM	human.			
REFERENCE				
AUTHORS	Homo sapiens			
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE				
AUTHORS	Waterston,R.H.			
TITLE	The sequence of Homo sapiens clone			
JOURNAL	Unpublished			
REFERENCE				
AUTHORS	Waterston,R.H.			
TITLE	Direct Submission			
JOURNAL	Submitted (10-MAR-2000) Genome Sequencing Center, Washington			
COMMENT	University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA			
	On Sep 1, 2000 this sequence version replaced gi:9954853.			
	----- Genome Center -----			
	Center: Washington University Genome Sequencing Center			
	Center code: WUGSC			
	Web site:http://genome.wustl.edu/gsc/index.shtml			
	----- Project Information -----			
	Center project name: H_NH0485B17			
	----- Summary Statistics -----			
	Sequencing vector: M13; 100%			
	Sequencing vector: plasmid; 0%			
	Chemistry: Dye-primer ET; 100% of reads			
	Assembly program: Phrap; version 0.990319			
	Consensus quality: 170599 bases at least Q40			
	Consensus quality: 173308 bases at least Q30			
	Consensus quality: 174949 bases at least Q20			
	Insert size: 187000; agarose-fp			
	Insert size: 178075; sum-of-contigs			
	Quality coverage: 4.89 in Q20 bases; agarose-fp			
	Quality coverage: 5.22 in Q20 bases; sum-of-contigs			

	* NOTE: This is a 'working draft' sequence. It currently			
	* consists of 23 contigs. The true order of the pieces			
	* is not known and their order in this sequence record is			
	* arbitrary. Gaps between the contigs are represented as			
	* runs of N, but the exact sizes of the gaps are unknown.			
	* This record will be updated with the finished sequence			
	* as soon as it is available and the accession number will			
	* be preserved.			

	* 1341: contig of 1341 bp in length			
	* 1342			
	* 1441: gap of unknown length			
	* 1442			
	* 2824: contig of 1383 bp in length			
	* 2825			
	* 2924: gap of unknown length			
	* 2925			
	* 4091: contig of 1167 bp in length			
	* 4092			
	* 4191: gap of unknown length			
	* 4192			
	* 5300: contig of 1109 bp in length			
	* 5301			
	* 5400: gap of unknown length			
	* 5401			
	* 6531: contig of 1131 bp in length			
	* 6532			
	* 6631: gap of unknown length			
	* 6632			
	* 7946: contig of 1315 bp in length			
	* 7947			
	* 8046: gap of unknown length			
	* 8047			
	* 9816: contig of 1770 bp in length			
	* 9817			
	* 9916: gap of unknown length			
	* 9917			
	* 11066: contig of 1150 bp in length			
	* 11067			
	* 11166: gap of unknown length			
	* 11167			
	* 12295: contig of 1129 bp in length			
	* 12296			
	* 12395: gap of unknown length			

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BASE COUNT 53372 a 37170 c 37454 g 50639 t 2224 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.4e-171;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGAGCTGTGAGCCGGGACTCGGGTCCCTGAGTCTGGATTCTTTCTCCGCTACT 60
DB 157680 CGCGCGGAGCTGTGAGCCGGGACTCGGGTCCCTGAGTCTGGATTCTTTCTCCGCTACT 157621
QY 61 GAGACACGCGGGTAGTCTCCACAGCAGATCAACTGGGAGTTGAAGTGTGAGTGAGAGT 120
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QY 121 GAAGAGAACACAGCAGGCTTCGGAGGGTTGTGTGCTCAGTCACTGAGAGTGAAGAGCC 180
DB 157560 GAAGAGAACACAGCAGGCTTCGGAGGGTTGTGTGCTCAGTCACTGAGAGTGAAGAGCC 157501
QY 181 CTCGAAGTCGTCCCTCTCATGCGGTCCACGCGCATGAGACCTTCTTGTCTCGTCACG 240
DB 157500 CTCGAAGTCGTCCCTCTCATGCGGTCCACGCGCATGAGACCTTCTTGTCTCGTCACG 157441
QY 241 GCATTAACCTAGGAGAGGAGGCGGAGGAGTGTGAGGGGCTCAGCGCAAGTGGCGTGC 300
DB 157440 GCATTAACCTAGGAGAGGAGGCGGAGGAGTGTGAGGGGCTCAGCGCAAGTGGCGTGC 157381
QY 301 TGTGGGGGTATCCGAGTCCCAAGACACCTGGAAACCCGACAGAAATTTCTGGACTCCC 360
DB 157380 TGTGGGGGTATCCGAGTCCCAAGACACCTGGAAACCCGACAGAAATTTCTGGACTCCC 157321
QY 361 CAGACGGGACAGGAGAGGAGCGGATGAGCG 392
DB 157320 CAGACGGGACAGGAGAGGAGCGGATGAGCG 157289

RESULT 6
AX245237
LOCUS AX245237 396 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 167 from Patent WO0166753.
ACCESSION AX245237
VERSION AX245237.1 GI:15859911
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 396)
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
Stache-Crain,B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0166753-A 167 13-SEP-2001.
FEATURES
LOCATION/Qualifiers
source
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BASE COUNT 82 a 97 c 146 g 71 t
ORIGIN

Query Match 50.1%; Score 391; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.4e-170;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGCGGAGCTGTGAGCCGGGACTCGGGTCCCTGAGTCTGGATTCTTTCTCCGCTACTG 61
DB 1 CGCGGAGCTGTGAGCCGGGACTCGGGTCCCTGAGTCTGGATTCTTTCTCCGCTACTG 60
QY 62 AGACACGCGGGTAGTCTCCACAGCAGATCAACTGGGAGTTGAAGTGTGAGTGAGAGT 121
DB 61 AGACACGCGGGTAGTCTCCACAGCAGATCAACTGGGAGTTGAAGTGTGAGTGAGAGT 120
QY 122 AAGAGGAACACAGCAGGCTTCGGAGGGTTGTGTGCTCAGTCACTGAGAGTGAAGGCC 181
DB 121 AAGAGGAACACAGCAGGCTTCGGAGGGTTGTGTGCTCAGTCACTGAGAGTGAAGGCC 180
QY 182 TCGAAGTCGTCTCCCTCTCATGCGGTCCACGCGCATGAGACCTTCTTGTCTCGTCACG 241
DB 181 TCGAAGTCGTCTCCCTCTCATGCGGTCCACGCGCATGAGACCTTCTTGTCTCGTCACG 240
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QY 302 GTTGGGGGTATCCGAGTCCCAAGACACCTGGAAACCCGACAGAAATTTCTGGACTCCC 361
DB 301 GTTGGGGGTATCCGAGTCCCAAGACACCTGGAAACCCGACAGAAATTTCTGGACTCCC 360
QY 362 AGACGGGACAGGAGAGGAGCGGATGAGCG 392
DB 361 AGACGGGACAGGAGAGGAGCGGATGAGCG 391

RESULT 7
AF251237
LOCUS AF251237 626 bp mRNA linear PRI 23-AUG-2000
DEFINITION Homo sapiens XAGE-1 mRNA, complete cds.
ACCESSION AF251237
VERSION AF251237.1 GI:9885324
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 626)
AUTHORS Liu,X.F., Helman,L.J., Yeung,C., Lee,B. and Pastan,I.
JOURNAL XAGE-1, A New Gene That is Frequently Expressed in Ewing's Sarcoma
TITLE Unpublished
REFERENCE 2 (bases 1 to 626)
AUTHORS Liu,X.F., Helman,L.J., Yeung,C., Lee,B. and Pastan,I.
JOURNAL Direct Submission
SUBMITTED (31-MAR-2000) Lab of Mol. Biol., NCI, NIH, 37 Convent Dr.
MSC 4255, Bethesda, MD 20892, USA
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LOCATION/Qualifiers
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BASE COUNT 194 a 153 c 170 g 109 t
ORIGIN
Query Match 49.9%; Score 390; DB 9; Length 626;
Best Local Similarity 100.0%; Pred. No. 6e-170;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match	49.4%	Score 386;	DB 9;	Length 463;	
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Qy	452	AAAAGAAGAACCCAGCAGCTGAAAGTCGGGATCTACACCTGGGCAGCAGACAGAGAAGA	511		
Db	138	AAAAGAAGAACCCAGCAGCTGAAAGTCGGGATCTACACCTGGGCAGCAGACAGAGAAGA	197		
Qy	512	TCAGGATACAGCTCAGATCCCAGTCCGCAGCATGGAAGGTGATCTGCAAGAGCTGCATCA	571		
Db	198	TCAGGATACAGCTCAGATCCCAGTCCGCAGCATGGAAGGTGATCTGCAAGAGCTGCATCA	257		
Qy	572	GTCAAACACCCGGGATAAATCTGGATTGGGTTCGGCGCTCAAGGTGAAGATAATACCTA	631		
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Qy	632	AAGAGGAACACTGTAAAATGCCAAGACAGGTGAAGAGCAACCAAGTTTAAATGAAGA	691		
Db	318	AAGAGGAACACTGTAAAATGCCAAGACAGGTGAAGAGCAACCAAGTTTAAATGAAGA	377		
Qy	692	CAAGCTGAACAACCGCAGCTGGTTTTATATTAGATTATTGCATTAACTATCTCAATAA	751		

Qy	752	AGTTTGCAGCTTTTCACCAAAAAA	777
Dd	438	AGTTTGCAGCTTTTCACCAAAAAA	463
RESULT	9		
LOCUS	AX062442	399 bp	DNA linear PAT 24-JAN-2001
DEFINITION	Sequence 69 from Patent WO0100828.		
ACCESSION	AX062442		
VERSION	AX062442.1	GI:12540317	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 399)		
JOURNAL	Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S., Carter,D., Reiter,M.W. and Mannion,J. Compositions and methods for the therapy and diagnosis of lung cancer		
FEATURES	Patent: WO 0100828-A 69 04-JAN-2001; CORIXA CORPORATION (US) Location/Qualifiers 1..399 /organism="Homo sapiens" /db_xref="taxon:9606"		
BASE COUNT	150 a	94 g	67 t
ORIGIN			1 others
	Query Match	48.7%	Score 380; DB 6; Length 399;
	Best Local Similarity	100.0%;	Pred. No. 3e-165;
	Matches 380; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
Qy	392	GACACACAACAACACAGAACCACACAGCCAGTGCCGAGGCCCGCCAGTAATGAGAGCCCCCA	451
Dd	10	GACACACAACAACACAGAACCACACAGCCAGTGCCGAGGCCCGCCAGTAATGAGAGCCCCCA	69
Qy	452	AAAGAAGAACCCAGCAGCTGAAGCTCGGGATCTCTACCTGGCAGCACAGACAGAAGAAGA	511
Dd	70	AAAGAAGAACCCAGCAGCTGAAGCTCGGGATCTCTACCTGGCAGCACAGACAGAAGAAGA	129
Qy	512	TCAGGATACAGCTGAGATCCCAGTGCGGGACATGGAAGGTGATCTGCAAGAGCTGCATCA	571

Db	130	TCAGGATACAGCTGAGATCCAGTCCAGTGCAGACATGGAAGGTGATCTGCAAGAGCTGCATCA	189
Qy	572	GTCAACACCGGGATAAATCTGGATTTGGTTCCGGCGTCAAGGTCAAGATTAATACCTA	631
Db	190	GTCAACACCGGGATAAATCTGGATTTGGTTCCGGCGTCAAGGTGAAGATTAATACCTA	249
Qy	632	AAGAGGAACACTGTAAATGCCAAGCAGGTGAAGAGCAACCAACAAAGTTTAAATGAAGA	691
Db	250	AAGAGGAACACTGTAAATGCCAAGCAGGTGAAGAGCAACCAACAAAGTTTAAATGAAGA	309
Qy	692	CAAGCTGAACACGCGAAGCTGTTTTATATTAGATATTTGACTTAACTATCTCAATAA	751
Db	310	CAAGCTGAACACGCGAAGCTGTTTTATATTAGATATTTGACTTAACTATCTCAATAA	369
Qy	752	AGTTTTCAGCTTTTCAACAA	771
Db	370	AGTTTTCAGCTTTTCAACAA	389
RESULT 10			
AX063163			
LOCUS	AX063163	Sequence 790 from Patent WO0100828.	457 bp DNA linear PAT 24-JAN-2001
DEFINITION	AX063163		
ACCESSION	AX063163		
VERSION	AX063163.1	GI:12541017	
KEYWORDS			
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
TITLE		Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,	
JOURNAL		Carter, D., Retter, M.W. and Mannion, J.	
FEATURES		Compositions and methods for the therapy and diagnosis of lung	
source		cancer	
PATENT		Patent: WO 0100828-A 790 04-JAN-2001;	
CORIXA		CORIXA CORPORATION (US)	
Location/Qualifiers			
1..457			
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
BASE COUNT	146 a	105 c	121 g 85 t
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Query Match	47.1%;	Score 368;	DB 6; Length 457;
Best Local Similarity	100.0%;	Pred. No. 1e-159;	
Matches	368;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	392	GACACACAAACACAGAACCCACAGCCAGTCCCGAGGAGCCAGTAATGGAGAGCCCA	451
Db	90	GACACACAAACACAGAACCCACAGCCAGTCCCGAGGAGCCAGTAATGGAGAGCCCA	149
Qy	452	AAAGAAGAACACAGCAGCTGAAAGTCGGGATCTACACCTGGCAGCAGACAGAGAAGA	511
Db	150	AAAGAAGAACACAGCAGCTGAAAGTCGGGATCTACACCTGGCAGCAGACAGAGAAGA	209
Qy	512	TCAGGATACAGCTGAGATCCCGAGTCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCA	571
Db	210	TCAGGATACAGCTGAGATCCCGAGTCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCA	269
Qy	572	GTCAACACCGGGATAAATCTGGATTTGGTTCCGGCGTCAAGTGAAGATAATACCTA	631
Db	270	GTCAACACCGGGATAAATCTGGATTTGGTTCCGGCGTCAAGTGAAGATAATACCTA	329
Qy	632	AAGAGGAACACTGTAAATGCCAAGCAGGTGAAGAGCAACCAACAAAGTTTAAATGAAGA	691
Db	330	AAGAGGAACACTGTAAATGCCAAGCAGGTGAAGAGCAACCAACAAAGTTTAAATGAAGA	389
Qy	692	CAAGCTGAACACGCGAAGCTGTTTTATATTAGATATTTGACTTAACTATCTCAATAA	751
Db	390	CAAGCTGAACACGCGAAGCTGTTTTATATTAGATATTTGACTTAACTATCTCAATAA	449
Qy	752	AGTTTTCG 759	

Db	450	AGTTTTCG 457	
RESULT 11			
HSA318879			
LOCUS	HSA318879	481 bp mRNA linear PRI 14-JAN-2002	
DEFINITION	Homo sapiens mRNA for XAGE-1d protein.		
ACCESSION	AJ318879		
VERSION	AJ318879.1	GI:18157207	
KEYWORDS		XAGE-1d gene.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
TITLE		Zendman, A.J.W., van Kraats, A.A., Weidle, U.H., Ruiter, D.R. and Van	
JOURNAL		Muijen, G.N.P.	
REFERENCE		Expression profile of members of the XAGE cancer/testis antigen	
AUTHORS		family	
TITLE			
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 481)	
AUTHORS		Zendman, A.J.W.	
TITLE		Direct Submission	
JOURNAL		Submitted (14-AUG-2001) Zendman A.J.W., Department of Pathology,	
FEATURES		University Medical Center St Radboud, Geert Grooteplein Zuid 24, PO	
source		Box 9101 6500 HB Nijmegen, NETHERLANDS	
Location/Qualifiers			
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/organism="Homo sapiens"			
/db_xref="taxon:9606"			
/chromosome="X"			
/map="Xp11.21-Xp11.22"			
/tissue="Ewing sarcoma"			
125..334			
/gene="XAGE-1d"			
125..334			
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/protein_id="CAC82987.1"			
/db_xref="GI:18157208"			
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LOELHQSNTGDKSGFGFRQGEDNT"			
BASE COUNT	163 a	107 c	127 g 84 t
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Query Match	31.4%;	Score 245;	DB 9; Length 481;
Best Local Similarity	100.0%;	Pred. No. 1.e-102;	
Matches	245;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	535	TGCGCGACATGGAGGTGATCTGCAAGAGCTGCATCAGTCAAAACACCGGGGATAATCTG	594
Db	237	TGCGCGACATGGAGGTGATCTGCAAGAGCTGCATCAGTCAAAACACCGGGGATAATCTG	296
Qy	595	GATTTGGTTCCCGCGTCAAGGTGAAGATAATACCTTAAGAGCAACACTGTAATAATGCCA	654
Db	297	GATTTGGTTCCCGCGTCAAGGTGAAGATAATACCTTAAGAGCAACACTGTAATAATGCCA	356
Qy	655	GAACAGGTGAAGAGCAACCAACCAAGTTTAAATGAAGCAACAGCTGAACCAACGCAAGCTGG	714
Db	357	GAACAGGTGAAGAGCAACCAACCAAGTTTAAATGAAGCAACAGCTGAACCAACGCAAGCTGG	416
Qy	715	TTTATATATGATATTTGACTTAACTATCTCAATAAAGTTTTCACCAAAAA	774
Db	417	TTTATATATGATATTTGACTTAACTATCTCAATAAAGTTTTCACCAAAAA	476
Qy	775	AAAAA 779	
Db	477	AAAAA 481	
RESULT 12			

AX063165
LOCUS AX063165 461 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 792 from Patent WO0100828.
ACCESSION AX063165
VERSION AX063165.1 GI:12541018
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 461)
AUTHORS Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S.,
Carter,D., Retter,M.W. and Mannion,J.
TITLE Compositions and methods for the therapy and diagnosis of lung
cancer
JOURNAL Patent: WO 0100828-A 792 04-JAN-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. .461
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 150 a 104 c 123 g 84 t
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Query Match 29.7%; Score 232; DB 6; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.2e-96;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 535 TCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATCTG 594
Db 230 TCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATCTG 289
Qy 595 GATTGGGTTCCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACTGTAAATGCCA 654
Db 290 GATTGGGTTCCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACTGTAAATGCCA 349
Qy 655 GAAGCAGTGAAGAGCAACACCAAGTTTAATGAAGCAAGCTGAAACACGCAAGCTGG 714
Db 350 GAAGCAGTGAAGAGCAACCAAGTTTAATGAAGCAAGCTGAAACACGCAAGCTGG 409
Qy 715 TTTTATATTAGATTGACCTTAACCTATCTCAATAAAGTTTTCAGCTTTTC 766
Db 410 TTTTATATTAGATTGACCTTAACCTATCTCAATAAAGTTTTCAGCTTTTC 461
RESULT 13
LOCUS AX062443 479 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 70 from Patent WO0100828.
ACCESSION AX062443
VERSION AX062443.1 GI:12540318
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 479)
AUTHORS Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S.,
Carter,D., Retter,M.W. and Mannion,J.
TITLE Compositions and methods for the therapy and diagnosis of lung
cancer
JOURNAL Patent: WO 0100828-A 70 04-JAN-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. .479
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 163 a 107 c 125 g 84 t
ORIGIN
Query Match 24.5%; Score 191; DB 6; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.3e-77;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 535 TCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATCTG 594
Db 232 TCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATCTG 291
Qy 595 GATTGGGTTCCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACTGTAAATGCCA 654
Db 292 GATTGGGTTCCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACTGTAAATGCCA 351
Qy 655 GAAGCAGTGAAGAGCAACACCAAGTTTAATGAAGCAAGCTGAAACACGCAAGCTGG 714
Db 352 GAAGCAGTGAAGAGCAACCAAGTTTAATGAAGCAAGCTGAAACACGCAAGCTGG 411
Qy 715 TTTTATATTAG 725
Db 412 TTTTATATTAG 422
RESULT 14
LOCUS AC016835 81953 bp DNA linear HTG 13-JUL-2000
DEFINITION Homo sapiens clone RP11-1P5, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC016835
VERSION AC016835.2 GI:9119883
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 81953)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-1P5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 81953)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArelizano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferret,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Gage,M.,
Galligan,J., Gardyna,S., Grant,G., Hagos,B., Heath,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tirrell,A., Vassiliev,H., Vo.A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (08-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6539374.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green,P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2520
Center clone name: L_P_5

* NOTE: This record contains 91 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that

* the record is updated, the accession number will
* be preserved.
* 1 769: contig of 769 bp in length
* 770 869: gap of 100 bp
* 870 1691: contig of 822 bp in length
* 1692 1791: gap of 100 bp
* 1792 2590: contig of 799 bp in length
* 2591 2690: gap of 100 bp
* 2691 3502: contig of 812 bp in length
* 3503 3602: gap of 100 bp
* 3603 4403: contig of 801 bp in length
* 4404 4503: gap of 100 bp
* 4504 5271: contig of 768 bp in length
* 5272 5371: gap of 100 bp
* 5372 6160: contig of 789 bp in length
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* 6261 7048: contig of 788 bp in length
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* 10680 10779: gap of 100 bp
* 10780 11545: contig of 766 bp in length
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* 18751 18850: gap of 100 bp
* 18851 19656: contig of 806 bp in length
* 19657 19756: gap of 100 bp
* 19757 20561: contig of 805 bp in length
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* 23307 23406: gap of 100 bp
* 23407 24217: contig of 811 bp in length
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* 25117 25216: gap of 100 bp
* 25217 25999: contig of 783 bp in length
* 26000 26099: gap of 100 bp
* 26100 26879: contig of 780 bp in length
* 26880 26979: gap of 100 bp
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* 28769 29592: contig of 824 bp in length
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* 34173 34272: gap of 100 bp
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* 37841 38651: contig of 811 bp in length
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* 38752 39566: contig of 815 bp in length
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* 39667 40472: contig of 806 bp in length
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* 41482 42296: contig of 815 bp in length
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* 42397 43213: contig of 817 bp in length
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* 43314 44124: contig of 811 bp in length
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* 56705 57487: contig of 783 bp in length
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* 58496 59302: contig of 807 bp in length
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* 59403 60205: contig of 803 bp in length
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* 60306 61119: contig of 814 bp in length
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* 63042 63857: contig of 816 bp in length
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* 64773 64872: gap of 100 bp

* 64873 65675: contig of 803 bp in length

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Best Local Similarity 100.0%; Pred. No. 1.8e-05;
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Db 56024 GATCCAACTGGGAGTTGAAGTGTGAGTGAGACTG 56057

RESULT 15
AC002415 93419 bp DNA linear HTG 12-AUG-1997
LOCUS Homo sapiens chromosome X clone BWXD142, *** SEQUENCING IN PROGRESS
DEFINITION ***; 6 unordered pieces.
ACCESSION AC002415
VERSION AC002415.1 GI:2323256
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 93419)
AUTHORS Chen,E., Brownstein,B.H., States,D.J., Schlessinger,D. and Mazzarella,R.
TITLE Direct Submission
JOURNAL Unpublished (1997)
REFERENCE 2 (bases 1 to 93419)
AUTHORS Brownstein,B.H., States,D.J. and Mazzarella,R.
TITLE Direct Submission
JOURNAL Washington University School of Medicine, Box 8232,
Louis, MO 63110, USA
COMMENT Current status of this project is available at:
'http://genome.wustl.edu/cgm/seq_projects.html'
Submitted by:
Elison Chen,
Advanced Center for Genetic Technology,
Applied Biosystems Division of Perlin Elmer Corp.,
850 Lincoln Center Drive,
Foster City, CA 94404 USA
e-mail: elison@genseq.apdbio.com
and
Buddy Brownstein,
Center for Genetics in Medicine,
Washington University School of Medicine, Box 8232
4566 Scott Avenue,
St. Louis, MO 63110, USA
e-mail: buddy@genetics.wustl.edu
and
David J. States,
Institute for Biomedical Computing
Washington University in St. Louis
700 South Euclid Ave.
St. Louis, MO 63108 USA
e-mail: states@ibc.wustl.edu.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 9560: contig of 9560 bp in length
* 9561 25127: contig of 15567 bp in length
* 25128 45675: contig of 20548 bp in length
* 45676 73399: contig of 27724 bp in length

* 73400 82075: contig of 8676 bp in length
* 82076 93419: contig of 11344 bp in length.
Location/Qualifiers
1. 93419
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/clone="BXND142"
BASE COUNT 25991 a 21189 c 20209 g 26030 t
ORIGIN

Query Match 4.4%; Score 34; DB 2; Length 93419;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 GATCCAACTGGGAGTTGAAGTGTGAGTGAGACTG 121
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Db 55823 GATCCAACTGGGAGTTGAAGTGTGAGTGAGACTG 55856

RESULT 16
AL445227 114344 bp DNA linear HTG 10-JUL-2001
LOCUS Homo sapiens chromosome X clone RP13-97115, *** SEQUENCING IN
DEFINITION PROGRESS ***; 6 unordered pieces.
ACCESSION AL445227
VERSION AL445227.7 GI:11611395
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 114344)
AUTHORS McIay,K.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Dec 9, 2000 this sequence version replaced gi:11493333.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: b97115
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 112482 bases at least Q40
Consensus quality: 113245 bases at least Q30
Consensus quality: 113597 bases at least Q20
Insert size: 113844; sum-of-contigs
Quality coverage: 5.91x in Q20 bases; agarose-fp
coverage: 5.72x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 13809: contig of 13809 bp in length
* 13810 13909: gap of 100 bp
* 13910 51507: contig of 37598 bp in length
* 51508 51607: gap of 100 bp
* 51608 65679: contig of 14072 bp in length
* 65680 65779: gap of 100 bp
* 65780 69064: contig of 3285 bp in length

/note="MIR repeat: matches 98. .247 of consensus"
14083. .14381
/note="AluX repeat: matches 1. .293 of consensus"
14906. .15126
/note="L2 repeat: matches 2364. .2569 of consensus"
15142. .15370
/note="MER4B repeat: matches 1. .215 of consensus"
15366. .16028
/note="MER4D repeat: matches 359. .1017 of consensus"
16097. .16211
/note="L2 repeat: matches 2631. .2749 of consensus"
16199. .16240
/note="L2 repeat: matches 2560. .2599 of consensus"
18264. .18349
/note="43 copies 2 mer ga 62% conserved"
19489. .19797
/note="AluJb repeat: matches 1. .306 of consensus"
19826. .20044
/note="L1M3 repeat: matches 5220. .5419 of consensus"
20045. .20175
/note="FLAM_A repeat: matches 1. .131 of consensus"
20176. .20249
/note="L1M3 repeat: matches 5419. .5496 of consensus"
20270. .20929
/note="L1MA5A repeat: matches 5447. .6104 of consensus"
20930. .21226
/note="AluX repeat: matches 1. .297 of consensus"
21227. .21417
/note="L1MA5A repeat: matches 6104. .6294 of consensus"
21418. .21461
/note="L1M4 repeat: matches 4295. .4338 of consensus"
21500. .23928
/note="L1PA5 repeat: matches 3696. .6143 of consensus"
24145. .24341
/note="L1MEC repeat: matches 1820. .2012 of consensus"
24385. .24681
/note="AluX repeat: matches 1. .296 of consensus"
24718. .28764
/note="L1PA4 repeat: matches 2108. .6144 of consensus"
28765. .28886
/note="FLAM_C repeat: matches 3. .124 of consensus"
28894. .28928
/note="L1PA4 repeat: matches 2064. .2097 of consensus"
28929. .29221
/note="AluSc repeat: matches 1. .296 of consensus"
29222. .29377
/note="L1MEC repeat: matches 2097. .2258 of consensus"
29428. .29551
/note="L2 repeat: matches 2621. .2749 of consensus"
29553. .29644
/note="AluJb repeat: matches 205. .296 of consensus"
29648. .30097
/note="MER87 repeat: matches 1. .469 of consensus"
30104. .30153
/note="25 copies 2 mer ca 76% conserved"
31811. .31976
/note="MIR repeat: matches 46. .204 of consensus"
32005. .32260
/note="128 copies 2 mer ta 80% conserved"
32903. .33194
/note="AluJo repeat: matches 1. .293 of consensus"
33677. .34221
/note="MER68A repeat: matches 1. .568 of consensus"
34372. .35093
/note="TIGGER1 repeat: matches 1650. .2308 of consensus"
35094. .35333
/note="L1PB1 repeat: matches 5909. .6155 of consensus"
35334. .35437
/note="TIGGER1 repeat: matches 2308. .2418 of consensus"
35477. .35878
/note="MLT1-INTERNAL repeat: matches 923. .1579 of
consensus"
36082. .36740

/note="MLT1-INTERNAL repeat: matches 201. .885 of
consensus"
36783. .37121
/note="L2 repeat: matches 824. .1219 of consensus"
37158. .37328
/note="L1M4 repeat: matches 4640. .4816 of consensus"
39953. .39978
/note="L3 copies 2 mer ca 100% conserved"
40525. .40566
/note="MIR repeat: matches 110. .151 of consensus"
44063. .44377
/note="AluJo repeat: matches 1. .299 of consensus"
44451. .45182
/note="MER21B repeat: matches 3. .790 of consensus"
45243. .45477
/note="L1M4 repeat: matches 4078. .4321 of consensus"
45515. .45890
/note="L1PA7 repeat: matches 5769. .6143 of consensus"
45900. .47783
/note="L1PA8 repeat: matches 4284. .6161 of consensus"
47776. .48115
/note="L1M4 repeat: matches 3680. .4029 of consensus"
48116. .48477
/note="MER47A repeat: matches 1. .365 of consensus"
48478. .48554

Query Match 4.4% Score 34; DB 9; Length 149749;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 GATCCAACTGGGAGTTGAAGTGTGAGTGAGAGTG 121
|||||
Db 95143 GATCCAACTGGGAGTTGAAGTGTGAGTGAGAGTG 95110

RESULT 18
AC002415/c
LOCUS
DEFINITION
ACCESSION AC002415
VERSION AC002415.1 GI:2323256
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 93419)
AUTHORS Chen, E., Brownstein, B.H., States, D.J., Schlessinger, D. and
Mazzarella, R.
TITLE Direct Submission
JOURNAL Unpublished (1997)
REFERENCE 2 (bases 1 to 93419)
AUTHORS Brownstein, B.H., States, D.J. and Mazzarella, R.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1997) Center for Genetics in Medicine, Box 8232,
Washington University School of Medicine, 4566 Scott Avenue, St.
Louis, MO 63110, USA
COMMENT Current status of this project is available at:
'http://genome.wustl.edu/cgm/seq_projects.html',
Submitted by:
Ellson Chen,
Advanced Center for Genetic Technology,
Applied Biosystems Division of Perlin Elmer Corp.,
850 Lincoln Center Drive,
Foster City, CA 94404 USA
e-mail: ellison@genseq.apldbio.com
and
Buddy Brownstein,
Center for Genetics in Medicine,
Washington University School of Medicine, Box 8232

4566 Scott Avenue.
St. Louis, MO 63110, USA
e-mail: buddygenetics.wustl.edu
and

David J. States,
Institute for Biomedical Computing
Washington University in St. Louis
700 South Euclid Ave.
St. Louis, MO 63108 USA

e-mail: states@bc.wustl.edu.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

* 1 9560: contig of 9560 bp in length
* 9561 25127: contig of 15567 bp in length
* 25128 45675: contig of 20548 bp in length
* 45676 73399: contig of 27724 bp in length
* 73400 82075: contig of 8676 bp in length
* 82076 93419: contig of 11344 bp in length.

FEATURES
source

1. .93419
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/clone="BXND142"

BASE COUNT 25991 a 21189 c 20209 g 26030 t
ORIGIN

Query Match 3.7%; Score 29; DB 2; Length 93419;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 ATCCAACTGGGAGTTGAAGTGTGAGTGAG 117
|||||
Db 1844 ATCCAACTGGGAGTTGAAGTGTGAGTGAG 1816

RESULT 19
AL445227/c 114344 bp DNA linear HTG 10-JUL-2001
LOCUS Homo sapiens chromosome X clone RP13-97I15, *** SEQUENCING IN
DEFINITION PROGRESS ***, 6 unordered pieces.

ACCESSION AL445227
VERSION AL445227.7 GI:11611395
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 114344)

McLay, K.
Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Dec 9, 2000 this sequence version replaced gi:11493333.
----- Genome Center

Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BB97I15
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 112482 bases at least Q40
Consensus quality: 113245 bases at least Q30
Consensus quality: 113597 bases at least Q20
Insert size: 113844; sum-of-contigs
Insert size: 122396; 9.8% error; agarose-fp
Quality coverage: 5.91x in Q20 bases; sum-of-contigs Quality
coverage: 5.72x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

* 1 13809: contig of 13809 bp in length
* 13810 13909: gap of 100 bp
* 13910 51507: contig of 37598 bp in length
* 51508 51607: gap of 100 bp
* 51608 65679: contig of 14072 bp in length
* 65680 65779: gap of 100 bp
* 65780 69064: contig of 3285 bp in length
* 69065 69164: gap of 100 bp
* 69165 101518: contig of 32354 bp in length
* 101519 101618: gap of 100 bp
* 101619 114344: contig of 12726 bp in length.

FEATURES
source

1. .114344
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RP13-97I15"
/clone_lib="RPC1-13.1"

misc_feature 1. .113809
/note="assembly_fragment:00241"
fragment_chain:1
clone_end:SP6
vector_side:left
13910..51507
/note="assembly_fragment:00680"
fragment_chain:1
51608..65679
/note="assembly_fragment:00207"
fragment_chain:1
65780..69064
/note="assembly_fragment:00300"
69165..101518
/note="assembly_fragment:01024"
101619..114344
/note="assembly_fragment:01825"
clone_end:T7
vector_side:right

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

BASE COUNT 32658 a 24338 c 24232 g 32616 t 500 others
ORIGIN

Query Match 3.7%; Score 29; DB 2; Length 114344;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 ATCCAACTGGGAGTTGAAGTGTGAGTGAG 117
|||||
Db 54734 ATCCAACTGGGAGTTGAAGTGTGAGTGAG 54706

RESULT 20

AL159987/c

LOCUS

DEFINITION

ACCESSION

VERSION

GI:13559998

Human DNA sequence from clone Rp11-167P23 on chromosome X, complete
sequence.

AL159987

AL159987.19 GI:13559998

AL159987 119024 bp DNA linear PRI 05-APR-2001
Human DNA sequence from clone Rp11-167P23 on chromosome X, complete
sequence.

AL159987 119024 bp DNA linear PRI 05-APR-2001
Human DNA sequence from clone Rp11-167P23 on chromosome X, complete
sequence.

AL159987 119024 bp DNA linear PRI 05-APR-2001
Human DNA sequence from clone Rp11-167P23 on chromosome X, complete
sequence.

KEYWORDS HTC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 119024)
Howden, P.
Direct Submission
Submitted (05-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Apr 6, 2001 this sequence version replaced gi:13274303.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30);
an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em., EMBL; Sw.,
SWISSPROT; Tr., TrEMBL; Wp., WormPep; Information on the WormPep
database can be found at
http://www.sanger.ac.uk/Projects/C-elegans/wormpep
This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/chrX
RP11-167P23 is from the library RPC1-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-167P23. It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP11-465E19 is at 118925 in this
sequence. The true right end of clone RP1-47K8 is at 100 in this
sequence.

FEATURES
Source
1..119024
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RP11-167P23"
/clone_lib="RPC1-11.1"
1..1665
repeat_region
/note="HERVL repeat: matches 1583..3249 of consensus"
repeat_region
1704..1743
/note="20 copies 2 mer ac 97% conserved"
repeat_region
1744..2134
/note="MLT2B repeat: matches 1..392 of consensus"
repeat_region
2381..2705
/note="AluJo repeat: matches 1..312 of consensus"
repeat_region
3061..3437
/note="RHEIC repeat: matches 1..371 of consensus"
repeat_region
3445..3470
/note="13 copies 2 mer tg 92% conserved"
repeat_region
4743..4916
/note="MIR repeat: matches 7..195 of consensus"
repeat_region
5565..5682
/note="MIR repeat: matches 101..213 of consensus"
misc_feature
9092..9323
/note="match: GSS: Em:AQ980738"
misc_feature
9325..9686
/note="match: GSS: Em:AQ980738"
misc_feature
complement(9528..9691)
/note="match: STS: Em:G06170"

repeat_region
9709..14228
/note="L1PA6 repeat: matches 1483..6143 of consensus"
misc_feature
14447..14834
/note="match: GSS: Em:AQ414791"
misc_feature
15106..15549
/note="match: GSS: Em:AQ559891"
misc_feature
15638..15846
/note="match: STS: Em:G03827"
repeat_region
16677..16718
/note="MIR repeat: matches 110..151 of consensus"
repeat_region
17584..17872
/note="AluSx repeat: matches 2..311 of consensus"
misc_feature
complement(18344..18789)
/note="match: GSS: Em:AF157981"
misc_feature
complement(18346..18734)
/note="match: GSS: Em:AQ720285"
misc_feature
complement(18439..18734)
/note="match: GSS: Em:AQ374048"
misc_feature
18737..19166
/note="match: GSS: Em:AQ359652"
repeat_region
19368..19398
/note="MER52C repeat: matches 1..31 of consensus"
repeat_region
19399..20564
/note="MER32A repeat: matches 42..1194 of consensus"
repeat_region
20559..20626
/note="MER52A repeat: matches 1684..1751 of consensus"
repeat_region
20828..21058
/note="AluJo repeat: matches 45..277 of consensus"
repeat_region
21379..21815
/note="MER66B repeat: matches 108..484 of consensus"
repeat_region
23053..23121
/note="L1MA5 repeat: matches 6225..6293 of consensus"
repeat_region
23381..23495
/note="MER41A repeat: matches 97..290 of consensus"
misc_feature
complement(23805..24380)
/note="match: GSS: Em:AQ507754"
misc_feature
complement(23964..24410)
/note="match: GSS: Em:AQ408397"
misc_feature
complement(23994..24399)
/note="match: GSS: Em:AQ508802"
misc_feature
complement(24134..24410)
/note="match: GSS: Em:AQ336100"
repeat_region
24485..25168
/note="L1PA13 repeat: matches 5475..6152 of consensus"
repeat_region
26042..26697
/note="L1M4 repeat: matches 2242..2926 of consensus"
repeat_region
26809..26927
/note="FLAM_C repeat: matches 1..119 of consensus"
repeat_region
26940..27076
/note="L1M4 repeat: matches 4992..5137 of consensus"
repeat_region
27380..27584
/note="MIR repeat: matches 62..262 of consensus"
repeat_region
27946..28065
/note="MER5A repeat: matches 68..188 of consensus"
repeat_region
28840..28923
/note="AluJ/FRAM repeat: matches 216..301 of consensus"
repeat_region
28943..29055
/note="FLAM_C repeat: matches 3..115 of consensus"
misc_feature
complement(29034..29436)
/note="match: GSS: Em:B52857"
misc_feature
complement(29901..30381)
/note="match: GSS: Em:AQ039266"
repeat_region
29989..30062
/note="HERVL40 repeat: matches 5295..5367 of consensus"
repeat_region
30081..30112
/note="16 copies 2 mer tg 100% conserved"
repeat_region
30144..30513
/note="MLT2FB repeat: matches 1..366 of consensus"
misc_feature
complement(31753..32234)
/note="match: GSS: Em:AQ209396"
repeat_region
31770..31935
/note="MIR repeat: matches 29..200 of consensus"
misc_feature
32266..32756

misc_feature	/note="match: GSS: Em:B47902"	Direct Submission	
32364..32727	/note="match: GSS: Em:AQ107228"	Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk	
repeat_region	32412..32777	requests: clonerequest@sanger.ac.uk	
repeat_region	/note="L1PA8 repeat: matches 5793..6159 of consensus"	On Mar 2, 2001 this sequence version replaced gi:13160313.	
repeat_region	32835..33112	During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.	
repeat_region	/note="L2 repeat: matches 2255..2522 of consensus"	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at	
misc_feature	33291..33584	http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at	
repeat_region	/note="MER39 repeat: matches 98..395 of consensus"	http://www.sanger.ac.uk/HGP/ChrX	
repeat_region	34330..34453	RP13-77011 is from the library RPCI-13.1 constructed by the group of Pieter de Jong. For further details see	
repeat_region	/note="FLAM_C repeat: matches 1..124 of consensus"	http://www.chori.org/bacpac/home.htm	
repeat_region	34597..34970	VECTOR: pBACe3.6	
repeat_region	/note="LTR3 repeat: matches 1..413 of consensus"	This sequence is the entire insert of clone RP13-77011 The true left end of clone RP13-97115 is at 15298 in this sequence. The true right end of clone RP13-97115 is at 131153 in this sequence.	
misc_feature	Complement(join(35694..36254,36581..36721))	Location/Qualifiers	
repeat_region	/note="match: GSS: Em:AQ389427"	1..149749	
repeat_region	36267..36573	/organism="Homo sapiens"	
repeat_region	/note="AluSc repeat: matches 1..309 of consensus"	/db_xref="taxon:9606"	
misc_feature	Complement(36574..36730)	/chromosome="X"	
repeat_region	/note="match: GSS: Em:AQ181456"	/map="p11.21-11.3"	
repeat_region	38336..38377	/clone="RP13-77011"	
repeat_region	/note="MIR repeat: matches 110..151 of consensus"	/clone_lib="RPCI-13.1"	
repeat_region	Complement(38817..39110)	18..1475	
repeat_region	/note="match: STS: Em:HS220XG1"	/note="L1MEL repeat: matches 3178..4658 of consensus"	
repeat_region	/note="L1 repeat: matches 4663..4779 of consensus"	1581..1842	
repeat_region	41765..41821	/note="L1MEL repeat: matches 4789..5069 of consensus"	
repeat_region	/note="L2 repeat: matches 1163..1219 of consensus"	1933..2226	
repeat_region	41849..42117	/note="AluSx repeat: matches 1..294 of consensus"	
repeat_region	/note="L2 repeat: matches 811..1102 of consensus"	2458..3266	
repeat_region	42146..42812	/note="L1MEL repeat: matches 5254..6148 of consensus"	
repeat_region	/note="MLT1-INTERNAL repeat: matches 201..885 of consensus"	3553..3584	
repeat_region	43013..43410	3835..4145	
repeat_region	/note="MLT1-INTERNAL repeat: matches 920..1322 of consensus"	/note="AluJb repeat: matches 1..310 of consensus"	
repeat_region	43499..43559	4173..4486	
repeat_region	/note="TIGER1 repeat: matches 2288..2359 of consensus"	/note="AluSx repeat: matches 1..312 of consensus"	
repeat_region	43560..43799	4982..5096	
repeat_region	/note="L1PB1 repeat: matches 5909..6155 of consensus"	/note="MLT2E repeat: matches 1..119 of consensus"	
repeat_region	43800..44089	5098..5254	
repeat_region	/note="TIGER1 repeat: matches 2078..2288 of consensus"	/note="AluSq repeat: matches 2..162 of consensus"	
repeat_region	44132..44550	5288..5529	
repeat_region	/note="TIGER1 repeat: matches 1650..2094 of consensus"	/note="L2 repeat: matches 2429..2705 of consensus"	
repeat_region	44701..45249	5597..5710	
repeat_region	/note="MER68A repeat: matches 1..568 of consensus"	/note="MIR repeat: matches 32..151 of consensus"	
repeat_region	45741..46034	6178..6471	
repeat_region	/note="AluJo repeat: matches 1..293 of consensus"	/note="AluSg repeat: matches 1..296 of consensus"	
repeat_region	46311..46342	7218..7504	
	/note="16 copies 2 mer ct 90% conserved"	/note="AluJo repeat: matches 2..302 of consensus"	
		7598..7692	
		/note="MIR repeat: matches 67..169 of consensus"	
		8791..9673	
		/note="cpg island"	
		/evidence=not_experimental	
Query Match	3.7%; Score 29; DB 9; Length 119024;		
Best Local Similarity	100.0%; Pred. No. 0.0033;		
Matches	29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	89 ATCCAACTGGGAGTTCAGTGTGAGTGG 117		
Db	18649 ATCCAACTGGGAGTTCAGTGTGAGTGG 18621		
RESULT	21		
AL445236			
LOCUS	AL445236 149749 bp DNA linear PRI 09-MAR-2001		
DEFINITION	Human DNA sequence from clone RP13-77011 on chromosome Xp11.21-11.3, complete sequence.		
ACCESSION	AL445236		
VERSION	AL445236.22 GI:13184376		
KEYWORDS	HTG.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 149749)		
AUTHORS	Howden,P.		

repeat_region /note="61 copies 2 mer ct 69% conserved"
repeat_region /note="21 copies 2 mer tt 85% conserved"
repeat_region /note="MER92C repeat: matches 272. .552 of consensus"
repeat_region /note="MER92B repeat: matches 2. .212 of consensus"
repeat_region /note="MIR repeat: matches 40. .154 of consensus"
repeat_region /note="MIR repeat: matches 63. .156 of consensus"
repeat_region /note="L2 repeat: matches 1779. .2341 of consensus"
repeat_region /note="L1M9 repeat: matches 6163. .6270 of consensus"
repeat_region /note="MIR repeat: matches 98. .247 of consensus"
repeat_region /note="AluX repeat: matches 1. .293 of consensus"
repeat_region /note="L2 repeat: matches 2364. .2569 of consensus"
repeat_region /note="MER4B repeat: matches 1. .215 of consensus"
repeat_region /note="MER4D repeat: matches 359. .1017 of consensus"
repeat_region /note="L2 repeat: matches 2631. .2749 of consensus"
repeat_region /note="L2 repeat: matches 2560. .2599 of consensus"
repeat_region /note="43 copies 2 mer ga 62% conserved"
repeat_region /note="AluB repeat: matches 1. .306 of consensus"
repeat_region /note="L1M3 repeat: matches 5220. .5419 of consensus"
repeat_region /note="FLAM.A repeat: matches 1. .131 of consensus"
repeat_region /note="L2 repeat: matches 5419. .5496 of consensus"
repeat_region /note="L1M5A repeat: matches 5447. .6104 of consensus"
repeat_region /note="AluX repeat: matches 1. .297 of consensus"
repeat_region /note="L1M5A repeat: matches 6104. .6294 of consensus"
repeat_region /note="L1M4 repeat: matches 4295. .4338 of consensus"
repeat_region /note="L1P5 repeat: matches 3696. .6143 of consensus"
repeat_region /note="L1MEC repeat: matches 1820. .2012 of consensus"
repeat_region /note="AluX repeat: matches 1. .296 of consensus"
repeat_region /note="L1P4 repeat: matches 2108. .6144 of consensus"
repeat_region /note="FLAM.C repeat: matches 3. .124 of consensus"
repeat_region /note="L1P4 repeat: matches 2064. .2097 of consensus"
repeat_region /note="AluSc repeat: matches 1. .296 of consensus"
repeat_region /note="L1MEC repeat: matches 2097. .2258 of consensus"
repeat_region /note="L2 repeat: matches 2621. .2749 of consensus"
repeat_region /note="AluB repeat: matches 205. .296 of consensus"
repeat_region /note="MER87 repeat: matches 1. .469 of consensus"
repeat_region /note="25 copies 2 mer ca 76% conserved"
repeat_region

repeat_region /note="MIR repeat: matches 46. .204 of consensus"
repeat_region /note="128 copies 2 mer ta 80% conserved"
repeat_region /note="AluJo repeat: matches 1. .293 of consensus"
repeat_region /note="MER68A repeat: matches 1. .568 of consensus"
repeat_region /note="TIGGER1 repeat: matches 1650. .2308 of consensus"
repeat_region /note="L1P1 repeat: matches 5909. .6155 of consensus"
repeat_region /note="TIGGER1 repeat: matches 2308. .2418 of consensus"
repeat_region /note="MULTI-INTERNAL repeat: matches 923. .1579 of consensus"
repeat_region /note="MULTI-INTERNAL repeat: matches 201. .885 of consensus"
repeat_region /note="L2 repeat: matches 824. .1219 of consensus"
repeat_region /note="L1M4 repeat: matches 4640. .4816 of consensus"
repeat_region /note="13 copies 2 mer ca 100% conserved"
repeat_region /note="MIR repeat: matches 110. .151 of consensus"
repeat_region /note="AluJo repeat: matches 1. .299 of consensus"
repeat_region /note="MER21B repeat: matches 3. .790 of consensus"
repeat_region /note="L1M4 repeat: matches 4078. .4321 of consensus"
repeat_region /note="L1P7 repeat: matches 5769. .6143 of consensus"
repeat_region /note="L1P8 repeat: matches 4284. .6161 of consensus"
repeat_region /note="L1M4 repeat: matches 3680. .4029 of consensus"
repeat_region /note="MER47A repeat: matches 1. .365 of consensus"
repeat_region /note="48478. .48554

Query Match 3.7%; Score 29; DB 9; Length 149749;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 ATCCAACTGGGAGTTGAAGTGTGAGTGTGAG 117
Db 76369 ATCCAACTGGGAGTTGAAGTGTGAGTGTGAG 76397

RESULT 22
LOCUS HSA318881 493 bp mRNA linear PRI 14-JAN-2002
DEFINITION Homo sapiens mRNA for XAGE-3 protein.
ACCESSION AJ318881
VERSION AJ318881.1 GI:18157211
KEYWORDS XAGE-3 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (slices)
AUTHORS Zendman,A.J.W., van Kraats,A.A., Weidie,U.H., Ruiters,D.R. and Van
Muijen,G.N.P.
TITLE Expression profile of members of the XAGE cancer/testis antigen
family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 493)
AUTHORS Zendman,A.J.W.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-2001) Zendman A.J.W., Department of Pathology,

University Medical Center St Radboud, Geert Grooteplein Zuid 24, PO
Box 9101 6500 HB Nijmegen, NETHERLANDS

FEATURES
source

1. .493
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="Xp11.21-Xp11.22"
/tissue.type="Ewing sarcoma"
61. .396
/gene="XAGE-3"
61. .396
/gene="XAGE-3"
/codon_start=1
/product="XAGE-3 protein"
/protein_id="CAC83008.1"
/db_xref="GI:18157212"
/translation="MIWGRSTYRPRRSVPPPELIGPMLPGDDEPQEPPTESR
DPAPQEREDQGAETQVPDLADLQELSQSKTGCGNGPDDQKILPKSEQFKMP
EGDGRQPV"
BASE COUNT 167 a 98 c 125 g 103 t
ORIGIN

Query Match 3.5%; Score 27; DB 9; Length 493;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 679 GTTTAAATGAAGACAGCTGAACAAC 705
|||||
Db 391 GTTTAAATGAAGACAGCTGAACAAC 417

RESULT 23
HSA318893
LOCUS
DEFINITION Homo sapiens XAGE-3 gene, exons 1-5.
ACCESSION AJ318893
VERSION AJ318893.1 GI:18181827
KEYWORDS XAGE-3 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
zendman,A.J.W., van Kraats,A.A., Weidle,U.H., Ruiter,D.J. and Van
Muijen,G.N.P.
Expression profile and alignment of the XAGE family of
cancer/testis associated genes
Unpublished
2 (bases 1 to 7200)
zendman,A.J.W.
Direct Submission
Submitted (15-AUG-2001) Zendman A.J.W., Department of Pathology,
University Medical Center, Geert Grooteplein Zuid 24, P.O. Box 9101
6500 HB Nijmegen, NETHERLANDS

FEATURES
source

1. .7200
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="Xp11.21-Xp11.22"
join(1282..1333,1442..1530,2045..2150,3683..3808,
5943..6052)
/gene="XAGE-3"
1282..6052
/gene="XAGE-3"
1282..1333
/gene="XAGE-3"
/number=1
1334..1441
/gene="XAGE-3"
/number=1
1442..1530

mRNA

gene

exon

intron

exon

CDS

/gene="XAGE-3"
/number=2
join(1450..1530,2045..2150,3683..3808,5943..5965)
/gene="XAGE-3"
/codon_start=1
/product="XAGE-3 protein"
/protein_id="CAC83014.1"
/db_xref="GI:18181828"
/translation="MIWGRSTYRPRRSVPPPELIGPMLPGDDEPQEPPTESR
DPAPQEREDQGAETQVPDLADLQELSQSKTGCGNGPDDQKILPKSEQFKMP
EGDGRQPV"
1531..2044
/gene="XAGE-3"
/number=2
2045..2150
/gene="XAGE-3"
/number=3
2151..3682
/gene="XAGE-3"
/number=3
3683..3808
/gene="XAGE-3"
/number=4
3809..5942
/gene="XAGE-3"
/number=4
5943..6052
/gene="XAGE-3"
/number=5
BASE COUNT 2131 a 1327 c 1573 g 2169 t
ORIGIN

Query Match 3.5%; Score 27; DB 9; Length 7200;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 679 GTTTAAATGAAGACAGCTGAACAAC 705
|||||
Db 5960 GTTTAAATGAAGACAGCTGAACAAC 5986

RESULT 24
AL590240
LOCUS
DEFINITION Human DNA sequence from clone RP11-26613 on chromosome X, complete
sequence.
ACCESSION AL590240 AC025380
VERSION AL590240.5 GI:13872461
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 130005)
Clark,S.
Direct Submission
Submitted (25-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On May 15, 2001 this sequence version replaced gi:8705130
gi:13785125.

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX> RP11-26613 is from the library RP11-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-26613 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-382F24 is at 129905 in this sequence. The true right end of clone RP1-296K21 is at 100 in this sequence.

FEATURES

source	Location/Qualifiers
	1..130005
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="X"
	/clone="RP11-26613"
	/clone_lib="RPC1-11.1"
	1..3875
repeat_region	/note="L1P repeat: matches 4..3892 of consensus"
repeat_region	4031..4472
repeat_region	/note="L1PA10 repeat: matches 5718..6165 of consensus"
repeat_region	4477..4658
repeat_region	/note="L1ME3A repeat: matches 5967..6157 of consensus"
repeat_region	4869..5170
repeat_region	/note="AluSc repeat: matches 1..306 of consensus"
repeat_region	6010..6307
repeat_region	/note="AluX repeat: matches 1..299 of consensus"
repeat_region	9580..9670
repeat_region	/note="MIR repeat: matches 127..214 of consensus"
repeat_region	10019..10387
repeat_region	/note="L1T1B repeat: matches 41..390 of consensus"
repeat_region	10424..11726
repeat_region	/note="L1W7 repeat: matches 4980..6284 of consensus"
repeat_region	12183..12372
repeat_region	/note="L1PA15 repeat: matches 5963..6153 of consensus"
repeat_region	12387..17012
repeat_region	/note="L1MA2 repeat: matches 1626..6308 of consensus"
repeat_region	17013..17325
repeat_region	/note="AluSq repeat: matches 1..313 of consensus"
repeat_region	17326..17971
repeat_region	/note="L1MA2 repeat: matches 979..1626 of consensus"
repeat_region	18003..24449
repeat_region	/note="L1PA7 repeat: matches 6..6143 of consensus"
repeat_region	24453..24926
repeat_region	/note="L1P repeat: matches 4190..4658 of consensus"
repeat_region	25188..25377
repeat_region	/note="L1MA repeat: matches 4619..4820 of consensus"
repeat_region	27242..27405
repeat_region	/note="82 copies 2 mer ta 76% conserved"
repeat_region	27731..27937
repeat_region	/note="L1MA repeat: matches 2..231 of consensus"
repeat_region	28628..28710
repeat_region	/note="AluJ/FLAM repeat: matches 2..84 of consensus"
repeat_region	28760..28926
repeat_region	/note="L1MA8 repeat: matches 6114..6290 of consensus"
repeat_region	30040..30466
repeat_region	/note="L1TR9 repeat: matches 198..625 of consensus"
repeat_region	30467..31208
repeat_region	/note="L1 repeat: matches 3291..4031 of consensus"
repeat_region	31209..31480
repeat_region	/note="AluX repeat: matches 38..311 of consensus"
repeat_region	31481..32418
repeat_region	/note="L1 repeat: matches 2350..3291 of consensus"
	32439..33203
	/note="L1PA13 repeat: matches 5395..6144 of consensus"
	33211..33753
	/note="L1P repeat: matches 1840..2380 of consensus"
	33748..35989
	/note="L1P repeat: matches 2006..4258 of consensus"
	35992..36688
	/note="L1PA3 repeat: matches 5449..6146 of consensus"
	36889..36728
	/note="20 copies 2 mer aa 80% conserved"
	36730..37022
	/note="L1P repeat: matches 1564..1858 of consensus"
	37018..37317
	/note="L1P4 repeat: matches 5312..5604 of consensus"
	37327..37629
	/note="AluX repeat: matches 1..303 of consensus"
	37630..37763
	/note="AluSg1 repeat: matches 2..133 of consensus"
	37782..38928
	/note="L1P4 repeat: matches 4190..5309 of consensus"
	39179..39381
	/note="L1M4 repeat: matches 4604..4820 of consensus"
	complement(40796..41371)
	/note="match: STS: Em:L30416"
	41220..41301
	/note="41 copies 2 mer tc 76% conserved"
	41260..41339
	/note="match: STS: Em:G09960 Em:G34497"
	42561..42643
	/note="AluJ/FLAM repeat: matches 2..84 of consensus"
	42693..42859
	/note="L1MA8 repeat: matches 6114..6290 of consensus"
	43973..44399
	/note="L1R3 repeat: matches 198..625 of consensus"
	44400..44975
	/note="L1P4 repeat: matches 3453..4031 of consensus"
	44980..46869
	/note="L1P3 repeat: matches 246..2016 of consensus"
	47559..47715
	/note="MIR repeat: matches 59..216 of consensus"
	48511..48672
	/note="L2 repeat: matches 2598..2750 of consensus"
	48814..48941
	/note="L1MD repeat: matches 177..303 of consensus"
	49219..49248
	/note="15 copies 2 mer tg 86% conserved"
	49262..49293
	/note="16 copies 2 mer ta 87% conserved"
	49387..49410
	/note="12 copies 2 mer ac 100% conserved"
	49711..50182
	/note="L2 repeat: matches 2252..2706 of consensus"
	50693..50992
	/note="AluY repeat: matches 10..299 of consensus"
	51042..51248
	/note="MIR repeat: matches 44..258 of consensus"
	51506..51944
	/note="L1MD2 repeat: matches 5686..6131 of consensus"
	51943..52075
	/note="L1MD3 repeat: matches 7590..7739 of consensus"
	53350..53652
	/note="AluSc repeat: matches 1..308 of consensus"
	54185..54326
	/note="MIR repeat: matches 117..261 of consensus"
	54859..55936
	/note="L1M1 repeat: matches 1825..2881 of consensus"
	55971..56980
	/note="L1PA5 repeat: matches 5130..6138 of consensus"
	56977..57337
	/note="L1P repeat: matches 4625..4985 of consensus"
	57369..57577
	/note="L1 repeat: matches 2958..3167 of consensus"
	57547..57704

```
/note="L1 repeat: matches 4465. .4628 of consensus"
57701. .58142
/note="L1MA4 repeat: matches 5662. .6185 of consensus"
58673. .58774
/note="L1MA8 repeat: matches 5573. .5661 of consensus"
58964. .59010
/note="L2 repeat: matches 1865. .1911 of consensus"
59415. .59702
/note="L1MA8 repeat: matches 5778. .6073 of consensus"
59704. .59857
/note="MER41B repeat: matches 482. .635 of consensus"
59860. .60918
/note="MER41-internal repeat: matches 3. .1717 of
consensus"
60942. .61207
/note="MER41-internal repeat: matches 985. .1277 of
consensus"
61204. .61802
/note="MER41-internal repeat: matches 3340. .3944 of
consensus"
61819. .62285
/note="MER41A repeat: matches 1. .467 of consensus"
62289. .62468
/note="L1MA8 repeat: matches 6059. .6243 of consensus"

Query Match      3.2%; Score 25; DB 9; Length 130005;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 CTGAAAGTCGGGATCTACACCTGG 493
|||||
Db 124239 CTGAAAGTCGGGATCTACACCTGG 124263

RESULT 25
LOCUS HSA318895 209 bp mRNA linear PRI 15-JAN-2002
DEFINITION Homo sapiens partial mRNA for XAGE-4 protein.
ACCESSION AJ318895
VERSION AJ318895.1 GI:18181831
KEYWORDS XAGE-4 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Zendenman,A.J.W., van Kraats,A.A., Weidie,U.H., Ruiter,D.J. and Van
Muijen,G.N.P.
TITLE Expression profile and alignment of the XAGE family of
cancer/testis associated genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 209)
AUTHORS Zendenman,A.J.W.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2001) Zendenman A.J.W., Department of Pathology,
University Medical Center, Geert Grooteplein Zuid 24, P.O. Box 9101
6500 HB Nijmegen, NETHERLANDS
FEATURES
source Location/Qualifiers
1. .209
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1. .209
/genes="XAGE-4"
CDS <1. .>209
/gene="XAGE-4"
/codon_start=3
/product="XAGE-4 protein"
/protein_id="CAC83092.1"
/db_xref="GI:18181832"
/translation="PPELIGPMLEPSDEEPQOEPTESROPTVPDPLETDLQELSQ
SKTGDCRCDGPDGKGIQPNQNLK"

BASE COUNT 64 a 51 c 55 g 39 t
ORIGIN
```

```
Query Match      3.1%; Score 24; DB 9; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 CTGAAAGTCGGGATCTACACCTG 492
|||||
Db 73 CTGAAAGTCGGGATCTACACCTG 96

RESULT 26
LOCUS AX246260 391 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 1190 from Patent WO0166753.
ACCESSION AX246260
VERSION AX246260.1 GI:15860934
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 391)
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,
Sidduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
Stache-Crain,B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0166753-A 1190 13-SEP-2001;
Chiron Corporation (US) ; Hyseq Inc. (US)
FEATURES
source Location/Qualifiers
1. .391
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 82 a 109 c 117 g 83 t
ORIGIN

Query Match      3.1%; Score 24; DB 6; Length 391;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 AGTGAGAGGCCCTCGAAGTCGTC 192
|||||
Db 169 AGTGAGAGGCCCTCGAAGTCGTC 192

RESULT 27
LOCUS AL158819/c 174913 bp DNA linear PRI 11-JAN-2001
DEFINITION Human DNA sequence from clone RP11-382F24 on chromosome X, complete
sequence.
ACCESSION AL158819
VERSION AL158819.14 GI:12214278
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 174913)
AUTHORS Wilson,S.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT On Jan 13, 2001 this sequence version replaced gi:12044561.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequencing map criteria
as follows. An attempt is made to resolve all sequencing problems,
```

such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX> RP11-382F24 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6

This sequence is the entire insert of clone RP11-382F24.

FEATURES

Source

```

1. 174913
   Location/Qualifiers
     organism="Homo sapiens"
     db_xref="taxon:9606"
     chromosome="X"
     clone="RP11-382F24"
     clone_lib="RPCI-11.2"
     size="5912"
     note="32 copies 2 mer tt 67% conserved"
repeat_region
6418..6716
   repeat_region
   /note="AluJo repeat: matches 1..290 of consensus"
6793..6859
   repeat_region
   /note="MER21B repeat: matches 731..789 of consensus"
6860..7118
   repeat_region
   /note="AluSc repeat: matches 37..295 of consensus"
7119..7245
   repeat_region
   /note="MER21B repeat: matches 574..731 of consensus"
7794..8080
   repeat_region
   /note="AluJo repeat: matches 1..287 of consensus"
8640..8865
   repeat_region
   /note="L2 repeat: matches 967..1225 of consensus"
8893..8991
   repeat_region
   /note="L1M4 repeat: matches 4639..4743 of consensus"
9069..9217
   repeat_region
   /note="L1M4 repeat: matches 4751..4919 of consensus"
10536..10704
   repeat_region
   /note="MIR repeat: matches 26..200 of consensus"
10864..11121
   repeat_region
   /note="MER21B repeat: matches 365..632 of consensus"
11183..12011
   repeat_region
   /note="L1 repeat: matches 2292..3139 of consensus"
12012..12311
   repeat_region
   /note="AluSq repeat: matches 1..299 of consensus"
12312..13246
   repeat_region
   /note="L1 repeat: matches 1392..2292 of consensus"
13591..13704
   repeat_region
   /note="MER4C repeat: matches 291..447 of consensus"
13770..13848
   repeat_region
   /note="MER4A2 repeat: matches 127..130 of consensus"
13833..14176
   repeat_region
   /note="MER4A repeat: matches 1..341 of consensus"
14193..16348
   repeat_region
   /note="MER4-internal repeat: matches 4087..6594 of consensus"
16349..16649
   repeat_region
   /note="AluY repeat: matches 1..302 of consensus"
16650..17319
   repeat_region
   /note="MER4-internal repeat: matches 3438..4087 of consensus"
17322..17446
   repeat_region
   /note="AluSq/x repeat: matches 13..138 of consensus"
17447..17740
   repeat_region
   /note="AluX repeat: matches 1..291 of consensus"
17742..18393
   repeat_region
   /note="MER4-internal repeat: matches 2738..3443 of consensus"
18395..18619
   repeat_region
   /note="LTR8 repeat: matches 1..257 of consensus"
18620..18816
   repeat_region
   /note="MER4-internal repeat: matches 2297..2495 of consensus"
18816..19398
   repeat_region
   /note="MER4-internal repeat: matches 1502..2072 of consensus"
19385..19499
   repeat_region
   /note="MER4-internal repeat: matches 1165..1274 of consensus"
19513..20234
   repeat_region
   /note="LIP3 repeat: matches 5424..6145 of consensus"
20244..20297
   repeat_region
   /note="L2 repeat: matches 2184..2238 of consensus"
20784..20826
   repeat_region
   /note="L1MD1 repeat: matches 6096..6138 of consensus"
20958..22064
   repeat_region
   /note="MER4-internal repeat: matches 1..1187 of consensus"
22067..22514
   repeat_region
   /note="MER4A2 repeat: matches 1..504 of consensus"
22515..22657
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   /note="MER4A2 repeat: matches 362..504 of consensus"
22931..23094
   repeat_region
   /note="MER31-internal repeat: matches 4396..6198 of consensus"
23172..23863
   repeat_region
   /note="LTR8 repeat: matches 1..669 of consensus"
23866..25428
   repeat_region
   /note="MER4-internal repeat: matches 4491..6100 of consensus"
25411..25599
   repeat_region
   /note="MER57-internal repeat: matches 4053..4244 of consensus"
25600..25896
   repeat_region
   /note="AluJo repeat: matches 5..305 of consensus"
25897..25883
   repeat_region
   /note="MER57-internal repeat: matches 1124..4053 of consensus"
27218..27643
   repeat_region
   /note="MER83-internal repeat: matches 1459..1887 of consensus"
27806..28561
   repeat_region
   /note="MER57-internal repeat: matches 1304..2095 of consensus"
29221..29355
   repeat_region
   /note="LTR8 repeat: matches 546..691 of consensus"
29376..29645
   repeat_region
   /note="L1PAL6 repeat: matches 5891..6157 of consensus"
30349..30999
   repeat_region
   /note="L1MC2 repeat: matches 5663..6330 of consensus"
31000..31162
   repeat_region
   /note="AluX repeat: matches 140..296 of consensus"
31163..31451
   repeat_region
   /note="AluSc repeat: matches 5..292 of consensus"
31452..31589
   repeat_region
   /note="AluX repeat: matches 1..140 of consensus"
31590..31844
   repeat_region
   /note="L1MC2 repeat: matches 5413..5663 of consensus"
31834..31854
   repeat_region
   /note="L1MC2 repeat: matches 5383..5403 of consensus"
31855..32527
   repeat_region
   /note="MER51B repeat: matches 1..617 of consensus"
32528..32943
   repeat_region
   /note="L1MC2 repeat: matches 5080..5383 of consensus"
32945..33237
   repeat_region
   /note="AluSq repeat: matches 1..294 of consensus"
33238..33289
   repeat_region
   /note="26 copies 2 mer ta 96% conserved"
33372..33395
   repeat_region
   /note="12 copies 2 mer at 95% conserved"
33400..33548
   repeat_region
   /note="L1MC2 repeat: matches 4927..5081 of consensus"

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repeat_region 34207..34429
/note="LIM8 repeat: matches 6026..6291 of consensus"
repeat_region 35255..36789
/note="LIM1 repeat: matches 4739..6304 of consensus"
repeat_region 36821..37775
/note="L1 repeat: matches 2350..3318 of consensus"
repeat_region 37795..38632
/note="L1P12 repeat: matches 5324..6159 of consensus"
repeat_region 38633..38934
/note="AluX repeat: matches 2..303 of consensus"
repeat_region 38935..40052
/note="L1P12 repeat: matches 4189..5324 of consensus"
repeat_region 40314..40494
/note="LIM4 repeat: matches 4619..4814 of consensus"
repeat_region 40643..40952
/note="AluY repeat: matches 1..310 of consensus"
repeat_region 41618..41895
/note="LIM3 repeat: matches 152..428 of consensus"
repeat_region 43027..43157
/note="LIM4 repeat: matches 89..231 of consensus"
repeat_region 43212..43271
/note="LIM4 repeat: matches 10..68 of consensus"
repeat_region 43949..44031
/note="AluJ/FLAM repeat: matches 2..84 of consensus"
repeat_region 44080..44238
/note="LIM8 repeat: matches 6114..6291 of consensus"
repeat_region 45104..45665
/note="LIM4 repeat: matches 3884..4482 of consensus"
repeat_region 45666..45950

Query Match 3.1%; Score 24; DB 9; Length 174913;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 679 GTTTAAATGAAGACAACTGAAC 702
|||||
Db 79541 GTTTAAATGAAGACAACTGAAC 79518

RESULT 28
AL450023 Human DNA sequence from clone RP11-552J9 on chromosome X, complete
LOCUS sequence.
DEFINITION AL450023
ACCESSION AL450023.21 GI:16580216
VERSION HTG.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 185532)
AUTHORS Bray-Allen, S.
JOURNAL Direct Submission
Submitted (02-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk
On Nov 1, 2001 this sequence version replaced gi:16214704.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations.
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em., EMBL; Sw.,

```

SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at
<http://www.sanger.ac.uk/Projects/C.elegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/ChrX>
 RP11-552J9 is from the library RPC1-11.2 constructed by the group of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6
 This sequence is the entire insert of clone RP11-552J9 The true left end of clone RP13-77011 is at 184976 in this sequence.

FEATURES

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source
1..185532
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RP11-552J9"
/clone_lib="RPC1-11.2"
38189..38197
misc_feature
/note="1329 bases of Tn10 transposon (J01829) removed here. This sequence represents the duplicated flanking sequence of the Tn10."
86440..86455
misc_feature
/note="Single clone region. Assembly confirmed by restriction digest data."
115370..115460
misc_feature
/note="Single clone region. Reads generated from a transposon library derived from a single pUC clone. Restriction digest data confirm the assembly."
BASE COUNT 51642 a 40741 c 40478 g 52671 t
ORIGIN

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Query Match 3.1%; Score 24; DB 9; Length 185532;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 31 CCTGAGGTCTGGATTCTTTCTCC 54
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Db 11271 CCTGAGGTCTGGATTCTTTCTCC 11294

RESULT 29
AX208978 214 bp DNA linear PAT 31-AUG-2001
LOCUS Sequence 818 from Patent WO0157207.
DEFINITION AX208978
ACCESSION AX208978
VERSION AX208978.1 GI:15423401
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 214)
AUTHORS Algate, P.A. and Mannion, J.
JOURNAL Compositions and methods for the therapy and diagnosis of ovarian cancer
Patent: WO 0157207-A 818 09-AUG-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
source
1..214
/organism="Homo sapiens"
/db_xref="taxon:9606"
74 a 34 c 55 g 51 t

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BASE COUNT 74 a 34 c 55 g 51 t
ORIGIN

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Query Match 2.9%; Score 23; DB 6; Length 214;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 645 TAAATGCCAGACAGGTGAAG 667
|||||

```

```
Db 122 TAAATGCCAGAGCAGGTGAAG 144
RESULT 30
AX198429
LOCUS AX198429 320 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 884 from Patent WO0151513.
ACCESSION AX198429
VERSION AX198429.1 GI:15388750
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 320)
AUTHORS Malyankar,U.M., Tchernev,V.T., Padigar,M., Taupier,R.J.,
TITLE Spytek,K.A., Majumder,K., Guo,X., Spaderna,S.K. and Boldog,F.L.
JOURNAL Polyptides and nucleic acids encoding same
PATENT: WO 0161009-A 7 23-AUG-2001;
FEATURES
LOCATION/Qualifiers
source 1..320
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 96 a 65 c 85 g 74 t
ORIGIN
Query Match 2.9%; Score 23; DB 6; Length 320;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 645 TAAATGCCAGAGCAGGTGAAG 667
|||||
Db 122 TAAATGCCAGAGCAGGTGAAG 144

RESULT 31
AX078298
LOCUS AX078298 580 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 102 from Patent WO0107471.
ACCESSION AX078298
VERSION AX078298.1 GI:13157989
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 580)
AUTHORS Hillman,J.L., Lai,P., Tang,Y.T., Yue,H., Au-Young,J., Bandman,O.,
TITLE Azimzai,Y., Yang,J., Lu,D.A., Baughn,M.R., Patterson,C. and Shah,P.
JOURNAL Cell cycle and proliferation proteins
PATENT: WO 0107471-A 102 01-FEB-2001;
FEATURES
LOCATION/Qualifiers
source 1..580
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 4764233CB1"
BASE COUNT 167 a 135 c 160 g 118 t
ORIGIN
Query Match 2.9%; Score 23; DB 6; Length 580;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 645 TAAATGCCAGAGCAGGTGAAG 667
|||||
Db 520 TAAATGCCAGAGCAGGTGAAG 542

RESULT 32
AX226501
LOCUS AX226501 611 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 7 from Patent WO0161009.
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ACCESSION AX226501
VERSION AX226501.1 GI:15555699
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 611)
AUTHORS Malyankar,U.M., Tchernev,V.T., Padigar,M., Taupier,R.J.,
TITLE Spytek,K.A., Majumder,K., Guo,X., Spaderna,S.K. and Boldog,F.L.
JOURNAL Polyptides and nucleic acids encoding same
PATENT: WO 0161009-A 7 23-AUG-2001;
FEATURES
LOCATION/Qualifiers
source 1..611
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 196 a 127 c 152 g 135 t
ORIGIN
Query Match 2.9%; Score 23; DB 6; Length 611;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 645 TAAATGCCAGAGCAGGTGAAG 667
|||||
Db 472 TAAATGCCAGAGCAGGTGAAG 494

RESULT 33
HSA318880
LOCUS HSA318880 620 bp mRNA linear PRI 14-JAN-2002
DEFINITION Homo sapiens mRNA for XAGE-2 protein.
ACCESSION AJ318880
VERSION AJ318880.1 GI:18157209
KEYWORDS XAGE-2 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Zendman,A.J.W., van Kraats,A.A., Weidle,U.H., Rulter,D.R. and Van
TITLE Muljen,G.N.P.
JOURNAL Expression profile of members of the XAGE cancer/testis antigen
REFERENCE 2 (bases 1 to 620)
AUTHORS Zendman,A.J.W.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-2001) Zendman A.J.W., Department of Pathology,
Box 9101 6500 HB Nijmegen, NETHERLANDS
FEATURES
LOCATION/Qualifiers
source 1..620
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="Xp11.21-Xp11.22"
/tissue_type="Ewing sarcoma"
189..524
/gene="XAGE-2"
189..524
/gene="XAGE-2"
/codon_start=1
/product="XAGE-2 protein"
/protein_id="CAC83007.1"
/db_xref="GI:18157210"
/translation="MSWGRSTYPRPRRSLOPPELGAMLEPTDEEPKEKPTKSR
NPTDQKRDDQGAETIQVPLEADQLCQTKTGDCGEGTDVKGKILPAHEFKMP
EAGEKRSQV"
BASE COUNT 191 a 131 c 156 g 142 t
ORIGIN
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Query Match	2.9%	Score 23:	DB 9;	Length 620;	
Best Local Similarity	100.0%	Pred. No. 9.6;			
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	645	TAAATGCCAGAGCAGGTGAAG 667			
Db	485	TAAATGCCAGAGCAGGTGAAG 507			
RESULT 34					
BC009232					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
REMARK					
COMMENT					
Query Match	2.9%	Score 23:	DB 9;	Length 620;	
Best Local Similarity	100.0%	Pred. No. 9.6;			
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	645	TAAATGCCAGAGCAGGTGAAG 667			
Db	485	TAAATGCCAGAGCAGGTGAAG 507			
RESULT 34					
BC009232					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
REMARK					
COMMENT					
Query Match	2.9%	Score 23:	DB 9;	Length 648;	
Best Local Similarity	100.0%	Pred. No. 9.5;			
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	645	TAAATGCCAGAGCAGGTGAAG 667			
Db	499	TAAATGCCAGAGCAGGTGAAG 521			
Query Match	2.9%	Score 23:	DB 9;	Length 648;	
Best Local Similarity	100.0%	Pred. No. 9.5;			
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	645	TAAATGCCAGAGCAGGTGAAG 667			
Db	499	TAAATGCCAGAGCAGGTGAAG 521			

ORIGIN

Query Match 2.9%; Score 23; DB 2; Length 220193;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 253 GAGCAAGGAGGCCGAGGAGTGG 275
|||||
Db 200939 GAGCAAGGAGGCCGAGGAGTGG 200961

RESULT 36

CEC33G3/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REMARK

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CEC33G3 33658 bp DNA linear INV 24-JAN-2002
Caenorhabditis elegans cosmid C33G3, complete sequence.
278540
278540.1 GI:1507775
HTG: Beta-mannosidase; Lys-tRNA; Transfer RNA.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (sites)
none.
Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)
99069613
The C.elegans Sequencing Consortium.
2 (bases 1 to 33658)
Matthews, L.
Direct Submission
Submitted (23-AUG-1996) Nematode Sequencing Project, Sanger
Institute, Hinxton, Cambridge CB10 1SA, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
available information.
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is not the entire insert of clone C33G3.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
The true left end of clone C33G3 is at 1 in this sequence. The true
right end of clone C33G3 is at 9942 in
sequence Z81064.
The true left end of clone F16B12 is at 33555 in this sequence. The
true right end of clone C04C11 is at 3475 in this sequence. The
start of this sequence (1..104) overlaps with the end of sequence
Z72501.
The end of this sequence (33555..33658) overlaps with the start of
sequence Z81064.
For a graphical representation of this sequence and its analysis
see:- [http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?](http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=C33G3)
name=C33G3

IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
overlap between neighbouring submissions.
location/Qualifiers
1..33658
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="X"
/clone="C33G3"
join(3893..4063,5154..5198,5368..5434,5705..5850,
6794..7084,7200..7334,7794..7946,7999..8247,8388..8884,
9084..9303,9350..9445,9581..9780,11849..11960)

FEATURES

source

gene

CDS

/gene="C33G3.1"
join(3893..4063,5154..5198,5368..5434,5705..5850,
6794..7084,7200..7334,7794..7946,7999..8247,8388..8884,
9084..9303,9350..9445,9581..9780,11849..11960)
/gene="C33G3.1"
/note="contains similarity to Pfam domain: PF00640
(Phosphotyrosine interaction domain (PTB/PID).),
Score=21.1, E-value=3.5e-05, N=1
cDNA EST yk259a5.5 comes from this gene"
/codon_start=1
/protein_id="CAB01738.2"
/db_xref="GI:6434268"
/db_xref="SPTREMBL:Q93325"
/translation="MIRFDPDESSESEKRFYYLRLMAKPGGKPIKTFVTWSRDED
VASASNTSDQLESQAMRVVITGOAFVCHVAQDMOEKHEDEAKSKISSQSEDE
AGNALDVIEERGREDSSSPMEAPPVGGPLYGKRLSLFOPRKPTTSSSGGTAI
DTTAIPNVEIETNSHTIIPRAPELVQLOFOTALPYOOKPQSLNLIQOQFNTLP
SOMPSTQTLPSLSENGQSHIPRMTPMPPNPYPATLPHRTWQALPYSPNMQSL
EONVPTYPQPMQLPSSSLPGLSPVMVSPYATLQLNMQSOQLDQHPQSGQITLM
DOYNLMRSQLDQAQSVQVAGCOVQLLRDQITSETTARLEAOSRTHOLISANRDL
PGSSIRLNYQVOPLADLRAGSLPPVKSKERRKDEGRTKTESNAEDTIDYSSSD
QYRTSNVMPKSFHILNMLPLVDINVPSCAAMSSRMEOFGMDGTICTSTPPKKEKK
PSSGILGENSRMSFNPGLGREKEROQQLMEFDTLEDSPRSIPSPSPSKAHNTTI
DSLFPKQDDPTIADREPQQLPPQSDQNKKNKTNVNLMTPTMPASSSLVTMYPPMR
QPAVPVNIQIPKVDVFRKTKTLTSLMDIAEPEPEPEPEPEPEPEPEPEPEPEPE
PPNPTDVEIKIEDYINRNVDRSKLPETSLTLRLTQAOQDNLGLNPGYQQ"
10280..10354
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/note="CTT Lys K-tRNA
predicted using tRNAscan-SE-1.11
preliminary prediction
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/product="tRNA-Lys"
10280..10354
/gene="C33G3.t1"
complement(11047..11121)
/gene="C33G3.t3"
/note="CTT Lys K-tRNA
predicted using tRNAscan-SE-1.11
preliminary prediction
similar to tRNA-Lys"
/product="tRNA-Lys"
complement(11047..11121)
/gene="C33G3.t3"
/gene="C33G3.t2"
complement(12554..12626)
/note="TTT Lys K-tRNA
predicted using tRNAscan-SE-1.11
preliminary prediction
similar to tRNA-Lys"
/product="tRNA-Lys"
complement(12554..12626)
/gene="C33G3.t2"
complement(13042..13243,13286..13400,13455..13560,
13607..13855,15236..15419,15543..15694,15803..15905,
16167..16285)
/gene="C33G3.3"
complement(join(13042..13243,13286..13400,13455..13560,
13607..13855,15236..15419,15543..15694,15803..15905,
16167..16285))
/gene="C33G3.3"
/note="predicted using Genefinder
Weak similarity to acetylcholine receptor alpha-7 chain
(SW:ACH7_HUMAN)
cDNA EST EMBL:Z14399 comes from this gene"
/codon_start=1
/protein_id="CAB01736.1"
/db_xref="GI:3874644"
/db_xref="SPTREMBL:Q93323"
/translation="MKEIQFNSSETSDLMQHEVNTLEOCLYYLAGESAKKLINIP
HAIASIPNLYSQQPTINFAQFTLOHFEHLKDISIHGYLELSHDDHLMNQDT
WKKNLVVSFHHINVPILGQSNPENHLKNGDAFEIRKVTETNOGNSAKVAFSLRTE

CDS

/gene="C33G3.3"
complement(join(13042..13243,13286..13400,13455..13560,
13607..13855,15236..15419,15543..15694,15803..15905,
16167..16285))
/gene="C33G3.3"
/note="predicted using Genefinder
Weak similarity to acetylcholine receptor alpha-7 chain
(SW:ACH7_HUMAN)
cDNA EST EMBL:Z14399 comes from this gene"
/codon_start=1
/protein_id="CAB01736.1"
/db_xref="GI:3874644"
/db_xref="SPTREMBL:Q93323"
/translation="MKEIQFNSSETSDLMQHEVNTLEOCLYYLAGESAKKLINIP
HAIASIPNLYSQQPTINFAQFTLOHFEHLKDISIHGYLELSHDDHLMNQDT
WKKNLVVSFHHINVPILGQSNPENHLKNGDAFEIRKVTETNOGNSAKVAFSLRTE


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CDDTDFENYNDVYKCCFSEPOQDREVIQFTSSGLPIFTDPKNFRDYGMVGSCTVPE
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MGLQPMTLIFSTRAPLASTPKPMRELAIFLNLISITTSIIIFCCMOVKRT
LPPWGRVTFQFANFLNGFLVNLISGVEEYNLDKYDEQVSONSYQKDWANVFAAAHVL
MGTISAIVIFVIVYCL"
Join(19807...19939,20519...20670,20805...21005,21238...21314,
21363...21496,21547...21801,21847...22151,22845...23146,
23258...23401,23445...23568,23613...23930,23987...24168,
24215...24329,24544...24804)
/genes="C33G3.4"
Join(19807...19939,20519...20670,20805...21005,21238...21314,
21363...21496,21547...21801,21847...22151,22845...23146,
23258...23401,23445...23568,23613...23930,23987...24168,
24215...24329,24544...24804)
/genes="C33G3.4"
/note="predicted using Genefinder
Similarity to Bovine beta-mannosidase (TR:G704360)
cDNA EST Yk23h3.3 comes from this gene
cDNA EST Yk26d5.3 comes from this gene
cDNA EST Yk23h3.5 comes from this gene
cDNA EST Yk26d5.5 comes from this gene
cDNA EST Yk44e10.5 comes from this gene
cDNA EST Yk128c10.3 comes from this gene
cDNA EST Yk134e12.5 comes from this gene
cDNA EST Yk159c11.5 comes from this gene
cDNA EST Yk177c7.5 comes from this gene
cDNA EST Yk159c11.3 comes from this gene
cDNA EST Yk177c7.3 comes from this gene
cDNA EST Yk476d8.3 comes from this gene
cDNA EST Yk476d8.5 comes from this gene
cDNA EST Yk4159g.3 comes from this gene
cDNA EST Yk4159g.5 comes from this gene"
/codon_start=1
/protein_id="CAB01737.1"
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GVPGDIVSLYASGIIDNPLPGENLNLKWAIEDDTYSRKFRILIDDDTVGAFLEI
ESVDITATVYNGKVLHNSNOFLPYHNVTDI IALGENDITIKFKSVKYAEKRADE
YKIFGHSLPDCNDPLVHGCHONFIRKAOYSEAWDGPSPFTVCIPISTLTINIRG
QTFHDNMTFRAHGWKVAFEFTFHGARTIEYSVQIPELGIESDYRLSATKSL
QTRSKNINSLIPMEHEPERMPNGSQKLDYDVVSMGQVKKRKGKTKVELVODL
IDPKPKGRNRYFKINDEPVLKGTNIPVSMFRSDINAKTEFLDSDVAEVMNA
IRVWGGFVSHNFYAYKSGKILVMQDLMFACALYPTTEF IQNAEEVSYNVDRIIS
QHTSVYSGNNEAAIAAGHMKASNTYESQVKDYLLYORLAKIAKVAPTIPFI
MSPSGNTEEGGVSKNPXYDYKGD.IHYNEFVNLNRDDTYLTPRCASEKSVQSYIP
MRETLNMINESDWEYTSKAMERHROHPGGIATNLLMIFQHLPIPAECGSKSVQSPS
CKTISASMSRLAYFSQVHQSIALKTQTLHYRRFRNTTNEGELNMCAMTQWLDV
WAAPTWTSTIDFQNMKAHYEARFFSNVAVSFADETDFNLKVFILNDPNYLLHNT
VNVQMLSWGNDPILTNFPHIDSVPAGSSEVLKTCITFSKITELSELYLYSTLYDSS
GVKIHEDVLVPLFPEVDNFTQDQISDVQRIDERTYILTITTDORVSPFWITCKKP
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complement(Join(24924...25150,25205...25435,26181...26264,
26308...26916,27080...27173,27220...27282))
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complement(Join(24924...25150,25205...25435,26181...26264,
26308...26916,27080...27173,27220...27282))
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/note="predicted using Genefinder"
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MSPSENAFTKLNGLLYSTKENVSVSHVPSPEHFRHSTDDDELDLVMYVKDHSF
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VLKQOLFHLILASRAYEYKFFKPMLEDNNRQKLLFEGRHLDSHNGTLSTSDTLEIN
2.8%; Score 22; DB 3; Length 33658;
Query Match
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

752 AGTTTTCAGCTTTCACCAAAA 773
QY
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|||||
Db 26926 AGTTTTCAGCTTTCACCAAAA 26905
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RESULT 37
AF143879 581 bp mRNA linear PRI 27-MAY-1999
LOCUS Homo sapiens clone IMAGE:120631 mRNA sequence.
DEFINITION AF143879
ACCESSION AF143879
VERSION AF143879.1 GI:4895021
KEYWORDS FLI_CDNA.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Persson,A.E., Lundeberg,J. and Uhlen,M.
TITLE EU-IMAGE: Full-insert length sequencing of human cDNA clones
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 581)
AUTHORS Persson,A.E., Lundeberg,J. and Uhlen,M.
TITLE Direct Submission
JOURNAL Submitted (19-APR-1999) Biochemistry and Microbiology,
Biotechnology, Royal Institute of Technology, Teknikringen 34,
Stockholm S-100 44, Sweden
FEATURES
Source
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Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Query Match 2.7%; Score 21; DB 9; Length 581;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 761 GCTTTCACCAAAAAA 781
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Db 553 GCTTTCACCAAAAAA 573
|||||
RESULT 38
HS5UL103HG 1665 bp DNA linear VRL 02-MAR-1995
LOCUS Murine cytomegalovirus UL103 homologue gene, complete cds, UL102
DEFINITION and UL104 homologue genes, partial cds.
ACCESSION L29246
VERSION L29246.1 GI:468306
KEYWORDS Murine cytomegalovirus (strain K181) DNA.
SOURCE Mouse cytomegalovirus 1
Organism: dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Muromegalovirus.
REFERENCE 1 (bases 1 to 1665)
AUTHORS Lyons,P.A., Ballas,B., Carrello,C., Shellam,G.R. and Scalzo,A.A.
TITLE Mapping and transcriptional analysis of the murine cytomegalovirus
homologue of the human cytomegalovirus UL103 open reading frame
JOURNAL Virology 204 (2), 835-839 (1994)
MEDLINE 95027718
FEATURES
Source
1..1665
Location/Qualifiers
/organism="Mouse cytomegalovirus 1"
/strain="K181"
/db_xref="taxon:10366"
<1..177
/note="UL102 homologue"
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/protein_id="AAA62598.1"
/db_xref="GI:688449"
/translation="ETTPGTANYRQPKQKTIPTTTPIGLPPPPSSAPEVSPRFRSPQOK
LETLDRNVQHLNG"
155..1108
CDS
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/note="UL103 homologue"
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/protein_id="AAA62599.1"
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ELINQAYRADSCRSFLEGCFLPFLDAEDALSELPLSSIRTKHRAVFRPKNTIDF
TLCMLLFAIETPLSROTLEHVLFTLGTPTGRLGTRMICKSCIKLVCTSLYLFFDET
DPTRTRIVPCTCMLYKETORQAQMLAEITYFGVODISSMLSVLTLDRVTKDGDVIG
DLAEVLNVCNVFYPLGTNGSVVTRWLSNNDNNPKRMYPTTTTDDTTTIPPTTK
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complement(1256..>1665)
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/translation="GRMVAVQPLDGLHNDICYNNDYKKTFFVLRVLEKVIIVLSOD
QTNFAVNSNGTEIDCVAIKOEVDVDDAIVSDTTGSDGLDAALRALRETTANTVGMVVE
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BASE COUNT 353 a 513 c 459 g 340 t
ORIGIN

Query Match 2.7%; Score 21; DB 14; Length 1665;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 TGATCTGCAAGAGCTGCATCA 571
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Db 573 TGATCTGCAAGAGCTGCATCA 593

RESULT 39
AC013875/c
LOCUS
DEFINITION
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pieces
ACCESSION
AC013875
VERSION
AC013875.1 GI:64337460
KEYWORDS
HTG; HTGS_PHASE2.
SOURCE
fruit fly.
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
Adams, M. and Venter, J.C.
Direct Submission
Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT
This sequence was identified as CDM:10213220 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
Source
1..9971
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
BASE COUNT 2516 a 2453 c 2501 g 2501 t
ORIGIN

Query Match 2.7%; Score 21; DB 2; Length 9971;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 393 ACACACACAAACACAGAACCA 413
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Db 9575 ACACACACAAACACAGAACCA 9555

RESULT 40
AC073266/c
LOCUS

Homo sapiens chromosome 19 clone RP11-393E18, WORKING DRAFT
SEQUENCE, 30 unordered pieces.
AC073266
VERSION
AC073266.3 GI:9795952
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
Waterston, R.H.
The sequence of Homo sapiens clone
2 (bases 1 to 200688)
Waterston, R.H.
Direct Submission
Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 11, 2000 this sequence version replaced gi:8920670.
COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0393E18
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 182974 bases at least Q40
Consensus quality: 187646 bases at least Q30
Consensus quality: 190053 bases at least Q20
Insert size: 168000; agarose-fp
Quality coverage: 5.50 in Q20 bases;
Quality coverage: 4.79 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1456: contig of 1456 bp in length
* 1457 1556: gap of unknown length
* 1557 3865: contig of 2309 bp in length
* 3866 3965: gap of unknown length
* 3966 5298: contig of 1333 bp in length
* 5299 5398: gap of unknown length
* 5399 7350: contig of 1952 bp in length
* 7351 7450: gap of unknown length
* 7451 8753: contig of 1303 bp in length
* 8754 10541: contig of 1688 bp in length
* 10542 12310: contig of 1669 bp in length
* 12311 12410: gap of unknown length
* 12411 14524: contig of 2114 bp in length
* 14525 14624: gap of unknown length
* 14625 16559: contig of 1934 bp in length
* 16560 16558: gap of unknown length
* 16559 18498: contig of 1840 bp in length
* 18499 18598: gap of unknown length
* 18599 21244: contig of 2646 bp in length
* 21245 21344: gap of unknown length
* 21345 23978: contig of 2634 bp in length
* 23979 24078: gap of unknown length
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* 24079 27768: contig of 3690 bp in length
* 27769 27868: gap of unknown length
* 27869 31566: contig of 3798 bp in length
* 31566 31766: gap of unknown length
* 31766 36499: contig of 4733 bp in length
* 36499 44328: gap of unknown length
* 44328 44328: contig of 7729 bp in length
* 44329 44328: gap of unknown length
* 44329 48785: contig of 4357 bp in length
* 48785 48886: gap of unknown length
* 48886 53682: contig of 4797 bp in length
* 53682 53783: gap of unknown length
* 53783 60898: contig of 7016 bp in length
* 60898 60899: gap of unknown length
* 60899 69529: contig of 8630 bp in length
* 69529 78413: gap of unknown length
* 78413 78513: contig of 8785 bp in length
* 78513 87228: gap of unknown length
* 87228 87329: contig of 8715 bp in length
* 87329 95401: contig of 8072 bp in length
* 95401 95501: gap of unknown length
* 95501 105284: contig of 9784 bp in length
* 105284 105385: gap of unknown length
* 105385 115645: contig of 10160 bp in length
* 115645 127535: gap of unknown length
* 127535 137337: contig of 11890 bp in length
* 137337 137438: gap of unknown length
* 137438 156915: contig of 19478 bp in length
* 156915 17311: gap of unknown length
* 17311 173312: contig of 16296 bp in length
* 173312 200688: gap of unknown length
* 173412 200688: contig of 2727 bp in length.

FEATURES
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                /db_xref="taxon:9606"
                /chromosome="19"
                /clone="RP11-393E18"
            1..1456
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            1557..3865
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            3966..5298
                /note="assembly_name:Contig12"
            5399..7350
                /note="assembly_name:Contig13"
            7451..8753
                /note="assembly_name:Contig14"
            8854..10541
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            10642..12310
                /note="assembly_name:Contig16"
            12411..14524
                /note="assembly_name:Contig17"
            14625..16558
                /note="assembly_name:Contig18"
            clone_end:17
                vector_side:left"
            16659..18498
                /note="assembly_name:Contig19"
            18599..21244
                /note="assembly_name:Contig20"
            21345..23978
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            24079..27768
                /note="assembly_name:Contig22"
            27869..31666
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            31767..36499
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misc_feature 44429..48785
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              vector_side:right"
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              /note="assembly_name:Contig27"
misc_feature 53783..60798
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misc_feature 69629..78413
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misc_feature 87329..95400
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BASE COUNT 60199 a 40808 c 41989 g 54792 t 2900 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 393 ACACACACAAACACACAGAACCA 413
   ||||| ||||| ||||| |||||
DB 69920 ACACACACAAACACACAGAACCA 69900

Search completed: October 16, 2002, 22:51:31
Job time : 2917 secs
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ORIGIN	Query Match 100.0%; Score 781; DB 6; Length 781; Best Local Similarity 100.0%; Pred. No. 5.2e-204; Matches 781; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	1 GCGGGGAGCTGTGAGCGGCGACTCGGGTCCCTGAGTCTTTCTCCGCTACT 60 	
Qy	61 GAGACACGGCGGTAGTCTCCACAGCAGATCCAAGTGGAGTGAAGTGTGAGTGAAGT 120 	
Db	61 GAGACACGGCGGTAGTCTCCACAGCAGATCCAAGTGGAGTGAAGTGTGAGTGAAGT 120 	
Qy	121 GAAGAGAACACAGCAGGCTTCCGGAGGTTGTGTGCTCAGTCACTCAGAGTGAGAAGGCC 180 	
Db	121 GAAGAGAACACAGCAGGCTTCCGGAGGTTGTGTGCTCAGTCACTCAGAGTGAGAAGGCC 180 	
Qy	181 CTCGAAGTCTGTCCTCTCATGCGGTGCCACGCCCATGACCTTCTGTCTGTCTCAGC 240 	
Db	181 CTCGAAGTCTGTCCTCTCATGCGGTGCCACGCCCATGACCTTCTGTCTGTCTCAGC 240 	
Qy	241 GCCATAACTAGGAGGAAGAGGCGCGAGGAGTGGAGGGCTCAGCGGAAGTGGGGTGC 300 	
Db	241 GCCATAACTAGGAGGAAGAGGCGCGAGGAGTGGAGGGCTCAGCGGAAGTGGGGTGC 300 	
Qy	301 TGTGGGGTATCCGAGTCCCAAGACAGCTGGAAACCCCGACAGAAGATCTTGGACTCCC 360 	
Db	301 TGTGGGGTATCCGAGTCCCAAGACAGCTGGAAACCCCGACAGAAGATCTTGGACTCCC 360 	
Qy	361 CAGACGGGACAGGAGAGGCGGATGAGCGACACACACAACACAGAACACACAGCC 420 	
Db	361 CAGACGGGACAGGAGAGGCGGATGAGCGACACACACAACACAGAACACACAGCC 420 	
Qy	421 AGTCCAGAGCCCGAGTAAATGAGAGCCCGCAAAAAGAGAACCCAGCTGAAGCTCGGG 480 	
Db	421 AGTCCAGAGCCCGAGTAAATGAGAGCCCGCAAAAAGAGAACCCAGCTGAAGCTCGGG 480 	
Qy	481 ATCTTACCTGGGACGACAGAGAGATCAGGATACAGTCAAGTCCAGTCCAGTCCGG 540 	
Db	481 ATCTTACCTGGGACGACAGAGAGATCAGGATACAGTCAAGTCCAGTCCAGTCCGG 540 	
Qy	541 ACATGAAGTGATCTGCAAGAGCTGCATCACTCAAAACACCGGGGATAAATCTGGATTG 600 	
Db	541 ACATGAAGTGATCTGCAAGAGCTGCATCACTCAAAACACCGGGGATAAATCTGGATTG 600 	
Qy	601 GGTTCGGGCTCAAGTGAAGATAATACCTAAAGAGGAACACTGTAAGTCCAGAGCA 660 	
Db	601 GGTTCGGGCTCAAGTGAAGATAATACCTAAAGAGGAACACTGTAAGTCCAGAGCA 660 	
Qy	661 GGTGAAGACCAACCAAGTTTAAATGAAGCAAGCTGAACCAAGCTGCTTTTAT 720 	
Db	661 GGTGAAGACCAACCAAGTTTAAATGAAGCAAGCTGAACCAAGCTGCTTTTAT 720 	
Qy	721 ATTAGATATTGCTTAACTATCTCAATAAAGTTTTCAGCTTTTCACCAAAAAA 780 	
Db	721 ATTAGATATTGCTTAACTATCTCAATAAAGTTTTCAGCTTTTCACCAAAAAA 780 	
Qy	781 A 781	
Db	781 A 781	
RESULT 2	HS318878	
LOCUS	HSA318878	
DEFINITION	Homo sapiens mRNA for XAGE-1c protein.	
ACCESSION	AJ318878	
VERSION	AJ318878.1 GI:18157205	
KEYWORDS	XAGE-1c gene.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

REFERENCE	Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (sites) Zendman, A.J.W., van Kraats, A.A., Weidie, U.H., Rulter, D.R. and Van Muijen, G.N.P.
TITLE	Expression profile of members of the XAGE cancer/testis antigen family
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 740)
AUTHORS	Zendman, A.J.W.
TITLE	Direct Submission
JOURNAL	Submitted (14-AUG-2001) Zendman A.J.W., Department of Pathology, University Medical Center St Radboud, Geert Grooteplein Zuid 24, PO Box 9101 6500 HB Nijmegen, NETHERLANDS
FEATURES	Location/Qualifiers
source	1..740 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="X" /map="Xp11.21-Xp11.22" /tissue_type="Ewing sarcoma" 163..645 /gene="XAGE-1c" 163..645 /gene="XAGE-1c" /codon_start=1 /product="XAGE-1c protein" /protein_id="CAC82986.1" /db_xref="GI:18157206" NP089770TGTGEGHERHTQTNHTASPRVMSPKKNOQLKVGILHLSHOK KIRIQLRSOCATWKVICKSCISOTPGINLDLGSVKVKIIPKEHCKMPEAGEQPOV
gene	
CDS	
BASE COUNT	224 a 170 c 216 g 130 t
ORIGIN	
Query Match	94.8%; Score 740; DB 9; Length 740;
Best Local Similarity	100.0%; Pred. No. 1e-192;
Matches	740; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	40 CTGATTTCTTCTCCGCTACTGACACACGGCGGTAGTCCACAGGAGGATCCAACTGGG 99
Db	1 CTGATTTCTTCTCCGCTACTGACACACGGCGGTAGTCCACAGGAGGATCCAACTGGG 60
Qy	100 AGTTGAAGTGTGAGTGAAGAGAACACAGCAGGCTTCCGGAGGGTGTGTGTGCTCA 159
Db	61 AGTTGAAGTGTGAGTGAAGAGAACACAGCAGGCTTCCGGAGGGTGTGTGTGCTCA 120
Qy	160 GTGACTCAGAGTGAGAGGCCCTCGAAGTGTGCTGCTCCTCTCATGCGGTGCCAGCCCAT 219
Db	121 GTGACTCAGAGTGAGAGGCCCTCGAAGTGTGCTGCTCCTCTCATGCGGTGCCAGCCCAT 18
Qy	220 GGACCTTCTTCTCCTCAGCGCCATAAATAGGGAGGAGGAGGCGCGAGGAGTGGAGGG 279
Db	181 GGACCTTCTTCTCCTCAGCGCCATAAATAGGGAGGAGGAGGCGCGAGGAGTGGAGGG 240
Qy	280 GCTCAGGCGAAGCTGGGGTGTGTTGGGGTATCCGAGTCCCAAGACACTTGAACCCC 339
Db	241 GCTCAGGCGAAGCTGGGGTGTGTTGGGGTATCCGAGTCCCAAGACACTTGAACCCC 300
Qy	340 GACAGAGATTCTGGACTCCCGACGCGGACACAGGAGGAGGCGCATGAGCGACACA 399
Db	301 GACAGAGATTCTGGACTCCCGACGCGGACACAGGAGGAGGCGCATGAGCGACACA 360
Qy	400 CAAACACAGAACACACAGCGAGTCCCGAGGAGCCAGTAATGGAGAGCCCAAAAAGAAG 459
Db	361 CAAACACAGAACACACAGCGAGTCCCGAGGAGCCAGTAATGGAGAGCCCAAAAAGAAG 420
Qy	460 AACACAGAGCTGAAGTGGGATCTTACACCTGGGACGACAGACAGAGATCAGGATA 519
Db	421 AACACAGAGCTGAAGTGGGATCTTACACCTGGGACGACAGACAGAGATCAGGATA 480
Qy	520 CAGCTGAGATCCCGAGTGGCGGACATGGAAGTGTATCTGCAAGAGCTGCATCAGTCAACA 579

Db	481	CAGCTGAGATCCCACTGCGCAGACATGGAAGGTGATCTCGAAGAGCTGCATCAGTCAACA	540
Qy	580	CCGGGGATAAATCTGGATTTCGGTTCGGCGCTCAAGGTGAAGATAATACTAAAGACGAA	639
Db	541	CCGGGGATAAATCTGGATTTCGGTTCGGCGCTCAAGGTGAAGATAATACTAAAGACGAA	600
Qy	640	CACGTGAAAATCCCAAGACAGCAGGTGAAGCAACACCAAGTTTAATCAAGACAACTGA	699
Db	601	CACGTGAAAATCCCAAGACAGCAGGTGAAGCAACACCAAGTTTAATCAAGACAACTGA	660
Qy	700	ACAACGCAAGCTGGTTTTATATTAGATATTGACTTTAAACTATCTCAATAAAGTTTTGC	759
Db	661	ACAACGCAAGCTGGTTTTATATTAGATATTGACTTTAAACTATCTCAATAAAGTTTTGC	720
Qy	760	AGCTTTCACCAAAAAA 779	
Db	721	AGCTTTCACCAAAAAA 740	
RESULT 3			
LOCUS	BC009538	529 bp mRNA linear	PK1 22-OCT-2001
DEFINITION	Homo sapiens, clone MGC:10063 IMAGE:3893227, mRNA, complete cds.		
ACCESSION	BC009538		
VERSION	BC009538.1	GI:16306934	
KEYWORDS	MGC.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Strausberg,R.		
JOURNAL	Submitted (29-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: DCTD/DPF/Gazdar cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.		
FEATURES	source	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 14 Row: g Column: 8. Location/Qualifiers 1..529 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="MGC:10063 IMAGE:3893227" /tissue_type="Lung, carcinoma, large cell undifferentiated." /clone_lib="NIH_MGC_69" /lab_host="DH10B" /note="Vector: pCMV-SPORT6" 184..429 /codon_start=1 /product="Unknown (protein for MGC:10063)" /protein_id="AAH09538.1" /db_xref="GI:16306935" /translation="MESPKKKQQLKVGILHLSGRKKIRIQLSQCATWKVICKSCI SOTPGINDLGSVKVKIIPKEEHCKMPEAGEEPQV"	
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ORIGIN	exon		

Query Match	67.3%	Score 526;	DB 9;	Length 529;
Best Local Similarity	100.0%;	Pred. No. 8e-134;		
Matches 526;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	256	GAAGAGAGGCGCAGAGGTGGAGGGGCTCAGCGAAGCTGTGGGGTATCCG	315	
Db	1	GAAGAGGCGCGAGGTGGAGGGGCTCAGCGAAGCTGTGGGGTATCCG	60	
Qy	316	AGTCCCAAGACCTTGAACCCCGACAGAAAGATTCTGGACTCCCGACGCGGACCA	375	
Db	61	AGTCCCAAGACCTTGAACCCCGACAGAAAGATTCTGGACTCCCGACGCGGACCA	120	
Qy	376	GAGGACCGGCATGAGCGACACACAAACACAGAACCAACAGCCAGTCCCGAGGACCA	435	
Db	121	GAGGACCGGCATGAGCGACACACAAACACAGAACCAACAGCCAGTCCCGAGGACCA	180	
Qy	436	GTAATGGAGAGCCCAAAAAGAACAGCAGCTGAAAGTCGGGATCCTACACCTGGGC	495	
Db	181	GTAATGGAGAGCCCAAAAAGAACAGCAGCTGAAAGTCGGGATCCTACACCTGGGC	240	
Qy	496	AGCAGACAGAAGAAGATCAGGATACAGTCCAGTCCAGTCCGCGACATGGAAGTGATC	555	
Db	241	AGCAGACAGAAGAAGATCAGGATACAGTCCAGTCCAGTCCGCGACATGGAAGTGATC	300	
Qy	556	TGCAAGAGCTGCATCAGTCAACACCCGGGGATAAATCTGGATTGGGTTCCGGCGTCAAG	615	
Db	301	TGCAAGAGCTGCATCAGTCAACACCCGGGGATAAATCTGGATTGGGTTCCGGCGTCAAG	360	
Qy	616	GTGAAGATAATACCTAAAGAGGAACACTGTAAATGCCAGAGCAGGTGAAGACAACCA	675	
Db	361	GTGAAGATAATACCTAAAGAGGAACACTGTAAATGCCAGAGCAGGTGAAGACAACCA	420	
Qy	676	CAAGTTTAAATGAAGACAAGCTGAAACAACCAAGCTGGTTTATATTAGATATTGACT	735	
Db	421	CAAGTTTAAATGAAGACAAGCTGAAACAACCAAGCTGGTTTATATTAGATATTGACT	480	
Qy	736	TAACTATCTCAATAAAGTTTTCAGCTTTCACCAAAAAA 781		
Db	481	TAACTATCTCAATAAAGTTTTCAGCTTTCACCAAAAAA 526		
RESULT 4				
LOCUS	HSA400997	6060 bp DNA linear	PRI 05-MAY-2001	
DEFINITION	Homo sapiens XAGE-1b gene for cancer/testis-associated protein XAGE-1b, exons 1-4.			
ACCESSION	AJ400997.1	GI:13992557		
VERSION	AJ400997			
KEYWORDS	cancer/testis-associated protein; XAGE-1b gene.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Zendman,A.J.W., van Kraats,A.A., Weidle,U.H., Ruiters,D.J. and Van Muijen,G.N.P.			
TITLE	XAGE-1b, a novel cancer/testis-associated gene, induced in melanoma metastases			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 6060)			
AUTHORS	zendman,A.J.W.			
TITLE	Direct Submission			
JOURNAL	Submitted (24-MAY-2000) Zendman A.J.W., Pathology, University Medical Center St. Radboud, Geert Grooteplein Zuid 24, Nijmegen, 6500 HB POBox 9101, NETHERLANDS			
FEATURES	source	Location/Qualifiers 1..6060 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="X" /map="Xp11.21-Xp11.22" /tissue_type="melanoma metastasis" 659..736		
		exon		

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Best Local Similarity 100.0%; Pred. No. 7;le-97;			
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CGCGCGGAGCTGTGAGCGCGGACTCGGGTCCCTGAGGTCGTGATCTTCTCCGCTACT	60
Db	665	CGCGCGGAGCTGTGAGCGCGGACTCGGGTCCCTGAGGTCGTGATCTTCTCCGCTACT	724
Qy	61	GAGACACGGCGGTAGGTCTCACAGCAGATCCAACTGGGAGTTGAAGTGTGAGTGAGAGT	120
Db	725	GAGACACGGCGGTAGGTCTCACAGCAGATCCAACTGGGAGTTGAAGTGTGAGTGAGAGT	784
Qy	121	GAAGAGGAACACGAGGCTTCCGAGGGTTGTGTGTCAGTGACTCAGAGTGAGAAGGCC	180
Db	785	GAAGAGGAACACGAGGCTTCCGAGGGTTGTGTGTCAGTGACTCAGAGTGAGAAGGCC	844
Qy	181	CTCGAAGTCGTCGCTCTCATCGGTGGCCAGCGCCCATGACCTTCTTGTCTCGTCACG	240
Db	845	CTCGAAGTCGTCGCTCTCATCGGTGGCCAGCGCCCATGACCTTCTTGTCTCGTCACG	904
Qy	241	GCCATACTAGGAGGAGGAGGCCCGCAGGAGTGGAGGGGCTCAGCGCAAGCTGGGGTGC	300
Db	905	GCCATACTAGGAGGAGGAGGCCCGCAGGAGTGGAGGGGCTCAGCGCAAGCTGGGGTGC	964
Qy	301	TGTTGGGGGTATCCGAGTCCAGAAACACCTGGAACCCACACAGAGATTCTGGACTCCC	360
Db	965	TGTTGGGGGTATCCGAGTCCAGAAACACCTGGAACCCACACAGAGATTCTGGACTCCC	1024
Qy	361	CAGACGGGACACGAGAGGACGCGCATGACGC	392
Db	1025	CAGACGGGACACGAGAGGACGCGCATGACGC	1056
RESULT 5			
AC025553/c			
LOCUS	AC025553	180859 bp	DNA linear HTG 01-SEP-2000

DEFINITION	Homo sapiens chromosome X clone RP11-485B17, WORKING DRAFT
ACCESSION	SEQUENCE, 23 unordered pieces.
VERSION	AC025553.5 GI:9958270
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	Waterston,R.H.
JOURNAL	The sequence of Homo sapiens clone
AUTHORS	Unpublished
REFERENCE	2. (bases 1 to 180859)
TITLE	Waterston,R.H.
JOURNAL	Direct Submission
AUTHORS	Submitted (10-MAR-2000) Genome Sequencing Center, Washington
TITLE	University School of Medicine, 4444 Forest Park Parkway, St. Louis,
JOURNAL	MO 63108, USA
COMMENT	On Sep 1, 2000 this sequence version replaced gi:9954853.
----- Genome Center -----	
Center: Washington University Genome Sequencing Center	
Center code: WUGSC	
Web site:http://genome.wustl.edu/gsc/index.shtml	
----- Project Information -----	
Center project name: H.NH0485B17	
----- Summary Statistics -----	
Sequencing vector: M13; 100%	
Sequencing vector: plasmid; 0%	
Chemistry: Dye-primer ET; 100% of reads	
Assembly: Dye-terminator Big Dye; 0% of reads	
Consensus quality: 170599 bases at least Q40	
Consensus quality: 173308 bases at least Q30	
Consensus quality: 174949 bases at least Q20	
Insert size: 187000; agarose-1p	
Insert size: 178075; sum-of-contigs	
Quality coverage: 4.89 in Q20 bases; agarose-1p	
Quality coverage: 5.22 in Q20 bases; sum-of-contigs	

* NOTE: This is a 'working draft' sequence. It currently	
* consists of 23 contigs. The true order of the pieces	
* is not known and their order in this sequence record is	
* arbitrary. Gaps between the contigs are represented as	
* runs of N, but the exact sizes of the gaps are unknown.	
* This record will be updated with the finished sequence	
* as soon as it is available and the accession number will	
* be preserved.	
*	1 1341: contig of 1341 bp in length
*	1342 1441: gap of unknown length
*	1442 2824: contig of 1383 bp in length
*	2825 2924: gap of unknown length
*	2925 4091: contig of 1167 bp in length
*	4092 4191: gap of unknown length
*	4192 5300: contig of 1109 bp in length
*	5301 5400: gap of unknown length
*	5401 6531: contig of 1131 bp in length
*	6532 7946: contig of 1315 bp in length
*	7947 8046: gap of unknown length
*	8047 9816: contig of 1770 bp in length
*	9817 9916: gap of unknown length
*	9917 11066: contig of 1150 bp in length
*	11067 11166: gap of unknown length
*	11167 12295: contig of 1129 bp in length
*	12296 12396: gap of unknown length
*	12396 13579: contig of 1184 bp in length
*	13580 13679: gap of unknown length
*	13680 15201: contig of 1522 bp in length
*	15202 15301: gap of unknown length
*	15301 16390: contig of 1089 bp in length
*	16391 16490: gap of unknown length

Thu Oct 17 09:19:22 2002

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* 16491 18667: contig of 2177 bp in length
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* 18768 20869: contig of 2102 bp in length
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* 23569 23669: gap of unknown length
* 23669 24252: contig of 584 bp in length
* 24253 28943: gap of unknown length
* 28943 29044: contig of 4591 bp in length
* 29044 37619: gap of unknown length
* 37620 37720: contig of 8576 bp in length
* 37720 49928: gap of unknown length
* 49928 50028: contig of 12208 bp in length
* 50028 69101: gap of unknown length
* 69101 69201: contig of 19073 bp in length
* 69201 90261: gap of unknown length
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Best Local Similarity 100.0%; Pred. No. 8.6e-97;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGGCGAGCTGTGAGCCGGGACTCGGGTCCCTGAGGCTCTGGATTCTTTCTCCGCTACT 60
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QY 61 GAGACACGGGGTAGTCCACAGGCAGATCCAACTGGGAGTTGAAGTGTGAGTGTGAGAGT 120
Db 157620 GAGACACGGGGTAGTCCACAGGCAGATCCAACTGGGAGTTGAAGTGTGAGTGTGAGAGT 157561
QY 121 GAAGAGAACCCAGAGCTTCCGGAGGGTTGTGTGTGCTAGTCTCAGAGTGTGAGAGAGGCC 180
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QY 181 CTGGAAGTCTGTCCTCTCATCGGTCGCCAGGCCCATGGACCTTCTTGTCTCTGTCTCAGC 240
Db 157500 CTGGAAGTCTGTCCTCTCATCGGTCGCCAGGCCCATGGACCTTCTTGTCTCTGTCTCAGC 157441
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QY 361 CAGACGGGACCCAGAGAGGAGCGCATGACGG 392
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AX245237 396 bp DNA linear PAT 28-SEP-2001
LOCUS
DEFINITION Sequence 167 from Patent WO0166753.
ACCESSION AX245237
VERSION AX245237.1 GI:15859911
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 396)
WILLIAMS,L.T., ESCOBEDO,J., INNIS,M.A., GARCIA,P.D.,
SUDDUTH-KLINGER,J., REINHARD,C., RANDAZZO,F., KENNEDY,G.C., POT,D.,
KASSAM,A., LAMSON,G., DRMANAC,R., CRKVENJAKOV,R., DICKSON,M.,
DRMANAC,S., LABAT,I., LESHKOWITZ,D., KITA,D., GARCIA,V. and
Stache-Crain,B.
Human genes and gene expression products
Patent: WO 0166753-A 167 13-SEP-2001;
Chiron Corporation (US); Hyseq Inc. (US)
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Query Match 50.1%; Score 391; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.1e-96;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CCGCGAGCTGTGAGCCGGGACTCGGGTCCCTGAGGCTCTGGATTCTTTCTCCGCTACTG 60
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Qy 62 AGACACGGCGGTAGGTCCACAGGAGATCCAACTGGGAGTTGAAGTGTGAGTGAGACTG 121
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DEFINITION AF251237
ACCESSION AF251237
VERSION AF251237.1 GI:9885324
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Liu,X.F., Helman,L.J., Yeung,C., Lee,B. and Pastan,I.
TITLE XAGE-1, A New Gene That is Frequently Expressed in Ewing's Sarcoma
JOURNAL Unpublished
AUTHORS Liu,X.F., Helman,L.J., Yeung,C., Lee,B. and Pastan,I.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2000) Lab of Mol. Biol., NCI, NIH, 37 Convent Dr.
MSC 4255, Bethesda, MD 20892, USA
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BASE COUNT 194 a 153 c 170 g 109 t
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Best Local Similarity 98.7%; Pred. No. 1.2e-96;
Matches 394; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 383 GGCATGAGCGACACACAAACACAGAACCCAGGCGAGTCCAGGAGCCAGCTAATGG 442
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Db 345 AGAAGAAGATCAGGATACAGCTGAGATCCAGTGGCGGACATGGAAGTGATCTGCAAGA 404
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RESULT 8
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LOCUS AX062442 Sequence 69 from Patent WO0100828. linear PAT 24-JAN-2001
DEFINITION AX062442
ACCESSION AX062442
VERSION AX062442.1 GI:12540317
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 399)
Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S.,
Carter,D., Retter,M.W. and Mannion,J.
TITLE Compositions and methods for the therapy and diagnosis of lung
cancer
JOURNAL Patent: WO 0100828-A 69 04-JAN-2001;
CORIXA CORPORATION (US)
FEATURES
source
location/Qualifiers
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BASE COUNT 150 a 87 c 94 g 67 t 1 others
ORIGIN

Query Match 50.0%; Score 390.6; DB 6; Length 399;
Best Local Similarity 98.5%; Pred. No. 1.5e-96;
Matches 393; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Qy 443 AGAGCCCCAAAAAGAACAGCAGCTGAAAGTCGGGATCCTACACCTGGGAGCAGAC 502
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Qy 623 TAATACCTAAAGAGAACACTGTAAATGCCAGAGCAGGTGAAGAGCAACCAAGTTT 682
Db 241 TAATACCTAAAGAGAACACTGTAAATGCCAGAGCAGGTGAAGAGCAACCAAGTTT 300
Qy 683 AAATGAACACAGCTGAAACCAACGAGCTGGTTTTATATATAGATATTTGACTTAAACTA 742

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LOCUS HSA318879 481 bp mRNA linear PRI 14-JAN-2002
DEFINITION Homo sapiens mRNA for XAGE-1d protein.
ACCESSION AJ318879
VERSION AJ318879.1 GI:18157207
KEYWORDS XAGE-1d gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Zandman,A.J.W., van Kraats,A.A., Weidle,U.H., Ruiter,D.R. and Van
Muijen,G.N.P.
TITLE Expression profile of members of the XAGE cancer/testis antigen
family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 481)
AUTHORS Zandman,A.J.W.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-2001) Zandman A.J.W., Department of Pathology,
University Medical Center St Radboud, Geert Grooteplein Zuid 24, PO
Box 9101 6500 HB Nijmegen, NETHERLANDS
FEATURES
source
1..481
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="Xp11.21-Xp11.22"
/tissue_type="Ewing sarcoma"
125..334
/gene="XAGE-1d"
125..334
/gene="XAGE-1d"
/codon_start=1
/product="XAGE-1d protein"
/protein_id="CAC82987.1"
/db_xref="GI:18157208"
/translation="MESPKKKNOOLKVGILHLSRQKKIRIQLRSQVLGRNRMDEGD
LQELHOSNTGDKSGFRRQEDNT"
BASE COUNT 163 a 107 c 127 g 84 t
ORIGIN
Query Match 46.5%; Score 363; DB 9; Length 481;
Best Local Similarity 94.9%; Pred. No. 5.9e-89;
Matches 392; Conservative 0; Mismatches 5; Indels 16; Gaps 1;
QY 383 GGCATGAGCGACACACACACAGAACACACAGCCAGTCCAGGAGCCAGTAATGG 442
Db 69 GACACGGCGACACACACACACACAGAACACACAGCCAGTCCAGGAGCCAGTAATGG 128
QY 443 AGAGCCCCAAAAGAGAACACAGCTGAAAGTCGGGATCCTACACCTGGGCAGCAGAC 502
Db 129 AGAGCCCCAAAAGAGAACACAGCTGAAAGTCGGGATCCTACACCTGGGCAGCAGAC 188
QY 503 AGAAGAAGATCAGGATACAGCTGAGATCCAG-----TGC CGCAGATGG 546
Db 189 AGAAGAAGATCAGGATACAGCTGAGATCCAGTTTTCAGGAGGAATGCGCGACATGG 248
QY 547 AAGGTGATCTGAAGAGCTGTCATAGTCAACACCGGGGATAAATCTGGATTGGGTTC 606
Db 249 AAGGTGATCTGAAGAGCTGTCATAGTCAACACCGGGGATAAATCTGGATTGGGTTC 308
QY 607 GCGTCAAGGTGAAGATTAATACCTAAAGAGGACACTGTAAATGCCAGAGCAGGTGAA 666
Db 309 GCGTCAAGGTGAAGATTAATACCTAAAGAGGACACTGTAAATGCCAGAGCAGGTGAA 368
QY 667 GAGCAACCAAGTTTAAATGAAGCAAGCTCAAAACAACGCAAGCTGTTTATATTAGA 726
Db 369 GAGCAACCAAGTTTAAATGAAGCAAGCTCAAAACAACGCAAGCTGTTTATATTAGA 428
QY 727 TATTTGACTTAACATATCTCAATAAAGTTTTCAGCTTTCACCAAAAAAAA 779
Db 429 TATTTGACTTAACATATCTCAATAAAGTTTTCAGCTTTCACCAAAAAAAA 481

RESULT 12
AX062443
LOCUS
DEFINITION Sequence 70 from Patent WO0100828.
ACCESSION AX062443
VERSION AX062443.1 GI:12540318
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 479)
AUTHORS Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedwick,T.S.,
Carter,D., Retter,M.W. and Mannion,J.
TITLE Compositions and methods for the therapy and diagnosis of lung
cancer
JOURNAL Patent: WO 0100828-A 70 04-JAN-2001;
CORIXA CORPORATION (US)
FEATURES
source
1..479
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 163 a 107 c 125 g 84 t
ORIGIN
Query Match 45.3%; Score 354; DB 6; Length 479;
Best Local Similarity 94.7%; Pred. No. 1.8e-86;
Matches 394; Conservative 0; Mismatches 5; Indels 17; Gaps 2;
QY 383 GGCATGAGCGACACACACACACAGAACACACAGCCAGTCCAGGAGCCAGTAATGG 442
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QY 443 AGAGCCCCAAAAGAGAACACAGCTGAAAGTCGGGATCCTACACCTGGGCAGCAGAC 502
Db 124 AGAGCCCCAAAAGAGAACACAGCTGAAAGTCGGGATCCTACACCTGGGCAGCAGAC 183
QY 503 AGAAGAAGATCAGGATACAGCTGAGATCCAG-----TGC CGCAGATGG 546
Db 184 AGAAGAAGATCAGGATACAGCTGAGATCCAGTCTGGGAAGGAAATGCGCGACATGG 243
QY 547 AAGGTGATCTGAAGAGCTGTCATAGTCAACACCGGGGATAAATCTGGATTGGGTTC 606
Db 244 AAGGTGATCTGAAGAGCTGTCATAGTCAACACCGGGGATAAATCTGGATTGGGTTC 303
QY 607 GCGTCAAGGTGAAGATTAATACCTAAAGAGGAACTGTAAATGCCAGAGCAGGTGAA 666
Db 304 GCGTCAAGGTGAAGATTAATACCTAAAGAGGAACTGTAAATGCCAGAGCAGGTGAA 363
QY 667 GAGCAACCAAGTTTAAATGAAGCAAGCTCAAAACAACGCAAGCTGTTTATATTAGA 725
Db 364 GAGCAACCAAGTTTAAATGAAGCAAGCTCAAAACAACGCAAGCTGTTTATATTAGA 423
QY 726 ATATTTGACTTAACATATCTCAATAAAGTTTTCAGCTTTCACCAAAAAAAA 781
Db 424 ATATTTGACTTAACATATCTCAATAAAGTTTTCAGCTTTCACCAAAAAAAA 479
RESULT 13
AX063165
LOCUS
DEFINITION Sequence 792 from Patent WO0100828.
ACCESSION AX063165
VERSION AX063165.1 GI:12541018
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 461)
AUTHORS Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedwick,T.S.,
Carter,D., Retter,M.W. and Mannion,J.

TITLE Compositions and methods for the therapy and diagnosis of lung cancer
JOURNAL Patent: WO 0100828-A 792 04-JAN-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..461
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 150 a 104 c 123 g 84 t
ORIGIN
Query Match 44.8%; Score 350; DB 6; Length 461;
Best Local Similarity 94.8%; Pred. No. 2.2e-85;
Matches 379; Conservative 0; Mismatches 5; Indels 16; Gaps 1;
QY 383 GGCATGAGCCACACACAAACACAGAACACACAGCCAGTCCCGAGGAGCCAGTAATGG 442
Db 62 GACAGGCGGACACACAAACACACAGAACACACAGCCAGTCCCGAGGAGCCAGTAATGG 121
QY 443 AGAGCCCAAAAGACAGACAGCCAGTGAAGTCCGGATCCTACACCTGGCGCAGCAGAC 502
Db 122 AGAGCCCAAAAGACAGACAGCCAGTGAAGTCCGGATCCTACACCTGGCGCAGCAGAC 181
QY 503 AGAAGAAGATCAGGATACAGCTGAGATCCCGAG-----TGCAGCAGCATGG 546
Db 182 AGAAGAAGATCAGGATACAGCTGAGATCCCGAGTGGGAAGGGAATGCGCGACATGG 241
QY 547 AAGGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATFAAATCTGATTTGGTTCC 606
Db 242 AAGGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATFAAATCTGATTTGGTTCC 301
QY 607 GGCCTCAAGTGAAGATATACCTAAAGAGAACACCTGTAAATGCCAGAAGCAGGTGAA 666
Db 302 GGCCTCAAGTGAAGATATACCTAAAGAGAACACCTGTAAATGCCAGAAGCAGGTGAA 361
QY 667 GAGCAACCAAGTTAAATGAAGACAGCTGAACACAGCAGCTGGTTTATATATAGA 726
Db 362 GAGCAACCAAGTTAAATGAAGACAGCTGAACACAGCAGCTGGTTTATATATAGA 421
QY 727 TATTGTACTTAACTATCTCAATAAAGTTTTCAGCTTTC 766
Db 422 TATTGTACTTAACTATCTCAATAAAGTTTTCAGCTTTC 461
RESULT 14
AX246260 391 bp DNA linear PAT 28-SEP-2001
LOCUS
DEFINITION Sequence 1190 from Patent WO0166753.
ACCESSION AX246260
VERSION AX246260.1 GI:15860934
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 391)
AUTHORS Williams,I.T., Escobedo,J., Innis,M.A., Garcia,P.D.,
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
Stache-Grain,B.
Human genes and gene expression products
Patent: WO 0166753-A 1190 13-SEP-2001;
Chiron Corporation (US) : Hyseq Inc. (US)
FEATURES Location/Qualifiers
source 1..391
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 82 a 109 c 117 g 83 t
ORIGIN
Query Match 39.1%; Score 305; DB 6; Length 391;
Best Local Similarity 88.2%; Pred. No. 5.4e-73;

Matches 343; Conservative 0; Mismatches 45; Indels 1; Gaps 1;
QY 2 CGCGGAGCTGTGAGCGCGGCACTCGGGTCCCTCAGGTCTGGATTCTTCTCCGCTACTG 61
Db 1 CTGCGGACCTGTGACCCGCGGCACTTGGGGCCCTGATGCTGGATTCTTCTCCGATACTG 60
QY 62 AGACACGCGGGTAGGTCCACAGGCA-GATCCAACTGGGAGTTGAAAGTGTGAGTGAGAGT 120
Db 61 AGACACGCGCGTAGGTCCACAGGCACTATCCAACTGGAAGTTGAGTGAGAGT 120
QY 121 GAAGAGGAACACGAGGCTTCCGGAGGTTGTGTGTCAGTGACTCAGAGTGAGAGGCC 180
Db 121 GAACAGGAACCTTCCGGGTTTCCGGAGGTTGTGTGCGCAGTGACTCAAAGTGAGAGGCC 180
QY 181 CTCGAAGTCGTCGTCCTCTCATCGGTGCGCACGCCCACTTCTTGTCTCGTCAAC 240
Db 181 CTCGAAGTCGTCCTCTCATCGGTGCGCGCCTCGCCCACTGCTCTTGTCTCGCTCG 240
QY 241 GCCATAACTAGGATGAAGAGGCGCGAGGAGTGGAGGGCTCAGGGGAAGCTGGGGTGC 300
Db 241 GTCATAACTAGGAGGAACGAGGGCCGAGGAGTGTAAAGGCTCACTCGAAGCTTGGGTGC 300
QY 301 TGTGGGGGTATCTGAGTCCAGAGACCTTGGAAACCCGACAGAGAGATTCTGACACTCC 360
Db 301 TGTGGGGGTATCTGAGTCCAGAGTCCCACTAGCACCTTGGAAACCCGACCTGAGACTCTGC 360
QY 361 CAGCGGACACGAGGAGGCGGACATGA 389
Db 361 CACAGGAACCCAGGAGAGGTACGCCATCA 389
RESULT 15
HSA318881 HSA318881 493 bp mRNA linear PRI 14-JAN-2002
LOCUS
DEFINITION Homo sapiens mRNA for XAGE-3 protein.
ACCESSION AJ318881
VERSION AJ318881.1 GI:18157211
KEYWORDS XAGE-3 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Zendman,A.J.W., van Kraats,A.A., Weidle,U.H., Rulter,D.R. and Van
Muijen,G.N.P.
TITLE Expression profile of members of the XAGE cancer/testis antigen
family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 493)
AUTHORS Zendman,A.J.W.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-2001) Zendman A.J.W., Department of Pathology,
University Medical Center St Radboud, Geert Grooteplein Zuid 24, PO
Box 9101 6500 HB Nijmegen, NETHERLANDS
FEATURES Location/Qualifiers
source 1..493
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/db_xref="taxon:9606"
/chromosome="X"
/map="Xp11.21-Xp11.22"
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61..396
/gene="XAGE-3"
61..396
/gene="XAGE-3"
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/product="XAGE-3 protein"
/protein_id="CAC83008.1"
/db_xref="GI:18157212"
/translation="MIWRGRSTYPRRBRSSVPPPELIGPMLPEDEBPQEPPTESR
DPAPQEREEDGGAETQVDPLEADLQELSQKTTGGCGNGPDDQKILPKSEQFKMP
EGGDRQPOV"
BASE COUNT 167 a 98 c 125 g 103 t

<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

This sequence is the entire insert of clone RP13-77011 The true left end of clone RP13-97115 is at 15298 in this sequence. The true right end of clone RP13-97115 is at 131153 in this sequence.

FEATURES

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location/Qualifiers
1..149749
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/chromosome="X"
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/clone_lib="RPC1-13.1"
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/note="L1ME1 repeat: matches 3178..4658 of consensus"

repeat_region

/note="L1ME1 repeat: matches 4789..5069 of consensus"

repeat_region

/note="AluSx repeat: matches 1..294 of consensus"

repeat_region

/note="L1ME1 repeat: matches 5254..6148 of consensus"

repeat_region

/note="L16 copies 2 mer ac 84% conserved"

repeat_region

/note="AluJb repeat: matches 1..310 of consensus"

repeat_region

/note="AluSx repeat: matches 1..312 of consensus"

repeat_region

/note="MLT2E repeat: matches 1..119 of consensus"

repeat_region

/note="AluSq repeat: matches 2..162 of consensus"

repeat_region

/note="L2 repeat: matches 2429..2705 of consensus"

repeat_region

/note="MIR repeat: matches 32..151 of consensus"

repeat_region

/note="AluSg repeat: matches 1..296 of consensus"

repeat_region

/note="AluJo repeat: matches 2..302 of consensus"

repeat_region

/note="MIR repeat: matches 67..169 of consensus"

misc_feature

/note="CpG island"

/evidence=not_experimental

repeat_region

/note="61 copies 2 mer ct 69% conserved"

repeat_region

/note="21 copies 2 mer tt 85% conserved"

repeat_region

/note="MER92C repeat: matches 272..552 of consensus"

repeat_region

/note="MER92B repeat: matches 2..212 of consensus"

repeat_region

/note="MIR repeat: matches 40..154 of consensus"

repeat_region

/note="MIR repeat: matches 63..156 of consensus"

repeat_region

/note="L2 repeat: matches 1779..2341 of consensus"

repeat_region

/note="L1MA9 repeat: matches 6163..6270 of consensus"

repeat_region

/note="MIR repeat: matches 98..247 of consensus"

repeat_region

/note="AluSx repeat: matches 1..293 of consensus"

repeat_region

/note="L2 repeat: matches 2364..2569 of consensus"

repeat_region

/note="MER84B repeat: matches 1..215 of consensus"

repeat_region

/note="MER4D repeat: matches 359..1017 of consensus"

repeat_region

/note="L2 repeat: matches 2631..2749 of consensus"

repeat_region

16199..16240

repeat_region

/note="L2 repeat: matches 2560..2599 of consensus"

repeat_region

/note="43 copies 2 mer ga 62% conserved"

repeat_region

/note="AluJb repeat: matches 1..306 of consensus"

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/note="L1M3 repeat: matches 5220..5419 of consensus"

repeat_region

/note="FLAM_A repeat: matches 1..131 of consensus"

repeat_region

/note="L1M3 repeat: matches 5419..5496 of consensus"

repeat_region

/note="L1MA5A repeat: matches 5447..6104 of consensus"

repeat_region

/note="AluSx repeat: matches 1..297 of consensus"

repeat_region

/note="L1MA5A repeat: matches 6104..6294 of consensus"

repeat_region

/note="L1M4 repeat: matches 4295..4338 of consensus"

repeat_region

/note="L1PA5 repeat: matches 3696..6143 of consensus"

repeat_region

/note="L1MEC repeat: matches 1820..2012 of consensus"

repeat_region

/note="AluSx repeat: matches 1..296 of consensus"

repeat_region

/note="L1PA4 repeat: matches 2108..6144 of consensus"

repeat_region

/note="FLAM_C repeat: matches 3..124 of consensus"

repeat_region

/note="L1PA4 repeat: matches 2064..2097 of consensus"

repeat_region

/note="AluSc repeat: matches 1..296 of consensus"

repeat_region

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repeat_region

/note="L2 repeat: matches 2621..2749 of consensus"

repeat_region

/note="AluJb repeat: matches 205..296 of consensus"

repeat_region

/note="MER87 repeat: matches 1..469 of consensus"

repeat_region

/note="25 copies 2 mer ca 76% conserved"

repeat_region

/note="MIR repeat: matches 46..204 of consensus"

repeat_region

/note="128 copies 2 mer ta 80% conserved"

repeat_region

/note="AluJo repeat: matches 1..293 of consensus"

repeat_region

/note="MER68A repeat: matches 1..568 of consensus"

repeat_region

/note="TIGGER1 repeat: matches 1650..2308 of consensus"

repeat_region

/note="L1PB1 repeat: matches 5909..6155 of consensus"

repeat_region

/note="TIGGER1 repeat: matches 2308..2418 of consensus"

repeat_region

/note="MLT1-INTERNAL repeat: matches 923..1579 of consensus"

repeat_region

/note="MLT1-INTERNAL repeat: matches 201..885 of consensus"

repeat_region

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repeat_region

/note="L1M4 repeat: matches 4640..4816 of consensus"

repeat_region

/note="13 copies 2 mer ca 100% conserved"

repeat_region

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repeat_region

/note="AluJo repeat: matches 1..299 of consensus"

repeat_region


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/note="match: GSS: Em:AQ039266"
29989..30062
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30081..30112
/note="16 copies 2 mer tg 100% conserved"
30144..30513
/note="MLT2FB repeat: matches 1..366 of consensus"
complement(31753..32234)
/note="match: GSS: Em:AQ209396"
31770..31935
/note="MIR repeat: matches 29..200 of consensus"
32266..32756
/note="match: GSS: Em:B47902"
32364..32727
/note="match: GSS: Em:AQ107228"
32412..32777
/note="LIPB8 repeat: matches 5793..6159 of consensus"
32835..33112
/note="L2 repeat: matches 2255..2522 of consensus"
33291..33584
/note="MER39 repeat: matches 98..395 of consensus"
34330..34453
/note="FLAM_C repeat: matches 1..124 of consensus"
34597..34970
/note="LTR3 repeat: matches 1..413 of consensus"
complement(join(35694..36254,36581..36721))
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36267..36573
/note="AluSc repeat: matches 1..309 of consensus"
complement(36574..36730)
/note="match: GSS: Em:AQ181456"
38336..38377
/note="MIR repeat: matches 110..151 of consensus"
complement(38817..39110)
/note="match: STS: Em:HS220XG1"
41596..41706
/note="L1 repeat: matches 4663..4779 of consensus"
41765..41821
/note="L2 repeat: matches 1163..1219 of consensus"
41849..42117
/note="L2 repeat: matches 811..1102 of consensus"
42146..42812
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consensus"
43013..43410
/note="MLT1-INTERNAL repeat: matches 920..1322 of
consensus"
43499..43559
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43560..43799
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43800..44089
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44132..44550
/note="TIGGER1 repeat: matches 1650..2094 of consensus"
44701..45249
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45741..46034
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46311..46342
/note="16 copies 2 mer ct 90% conserved"
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Best Local Similarity 72.7%; Pred. No. 8.6e-37;
Matches 272; Conservative 0; Mismatches 85; Indels 17; Gaps 3;
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QY 14 GAGCCGGGACATCGGGTCCCTGAGTCTGGATCTTTCTCCGCTACTGAGACACGGCGG 73
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DB 18724 GAGCTGTGAGGTCAAGTTCCTGAGTCTGATCTTCTCTCTCTACTGAGACGACGAG 18665
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QY 74 TAGGTCACAGCAGACATCCAACTGGGAGTTGAGTGTGAGTGTGAGAGTGAAGAGAACCCAG 133
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Db 18664 TAGGTCACAGCAGCAGTCCAACTGGGAGTTGAAAGTTGAGTGAGGTTGAGGAGGAGCCAG 18605
QY 134 CAGGCTTCGAGAGGTTGT---GTGGTCAGTCACTCAGAGTGAGAGGCCCTCGAAGTCG 190
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Db 18604 CAGGCTTCGAGAGGTTGTCATCAGGGGGGAGGAGACTCAGAGGGAGAGGGCTCGAGGTCT 18545
QY 191 TCGTCCCTCTCATCGGTCGCCAGCCCATGGACCTTCTTGTCTGTCACGGCCATACATA 250
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Db 18544 TCATCCTTTTCACATGGCCGCCACAGCCAGGGGCTTCTT---TTTGTGACGGGCCACAATA 18486
QY 251 GGAGGAAAGGAGGGCCGAGGAGTGGAGGGCTCAGCGGAAGCTG-----GGG 297
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Db 18485 GGAAGGAAGGAGGGCCCTTGGCCAAAGGGGATCGGTTAAATGGGCACGCTGTTGTGGG 18426
QY 298 TCGTGTGGGGTATCCGAGTCCCAAGACACCTGGAACCCCGACACAGATTTCTGGACT 357
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Db 18425 TCGTGTGGAGGTATCTGAGTCCCAAGAAATGCTCAACACATCAGAGATATCCAGTGA 18366
QY 358 CCCCACACGGGACC 371
Db 18365 CTCCTCCAGGAGC 18352

RESULT 25
AX078298
LOCUS AX078298 580 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 102 from Patent WO0107471.
ACCESSION AX078298
VERSION AX078298.1 GI:13157989
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 580)
AUTHORS Hillman,J.L., Lai,P., Tang,Y.T., Yue,H., Au-Young,J., Bandman,O.,
Azizmaiz,Y., Yang,J., Lu,D.A., Baughn,M.R., Patterson,C. and Shah,P.
TITLE Cell cycle and proliferation proteins
JOURNAL Pat'ent: WO 0107471-A 102 01-FEB-2001;
Incyte Genomics, Inc. (US)
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Location/Qualifiers
source 1..580
/organism="Homo sapiens"
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/note="Incyte ID No: 4764233CB1"
BASE COUNT 167 a 135 c 160 g 118 t
ORIGIN
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Matches 216; Conservative 0; Mismatches 35; Indels 1; Gaps 1;
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QY 429 GAGCCCACTAATGGAGAGCCCAAGAAAGAACAGCAGCTGAAAGTCGGGATCCTACA 488
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Db 305 GAACCCACTGTAGAGAGCCTTAACAAGAGAACCACCCACTAAAGTCGGGATCCTACA 364
QY 489 CTTGGGACAGACAGAGAAGATCAGGATACAGTCCAGTCCCGAGCGGACATGCAA 548
|||||
Db 365 CTTGATCAGACAGAGAAGATGATCAGGTGTCAGCTGAGATTCAGTCCCTGACCTGGAA 424
QY 549 GTGTATCTGCAAGAGCTGCATCAGTCAACACCCGGGATAAATCTGGATTTGGGTTCCGG 608
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Db 425 GCCGATCTCCAGGAGCTATGTGACACAAGACTGGGGATGGATGTGAAGGT--GGTACTGA 483
QY 609 COTCAAGTGAAGATAATACCTAAAGAGGAACACTGTAAAATGCCAGAGCAGGTGAAGA 668
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Db 484 TGTCAAGGGAAGATTCTACCAAAAAGCAGACACTTTAAAATGCCAGAAGCAGGTGAAG 543
QY 669 GCACCCACAAGTTTAAATGAAGACAGCTGAACACAC 705
|||||
Db 544 GAAATCACAGGTTTAAAGGAAGATAAGCTGAACACAC 580
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* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

*	13810	13909:	contig of 13809 bp in length
*	13810	13909:	gap of 100 bp
*	13910	51567:	contig of 37538 bp in length
*	13910	51567:	gap of 100 bp
*	13908	65679:	contig of 14072 bp in length
*	13908	65779:	gap of 100 bp
*	6580	69064:	contig of 3285 bp in length
*	6580	69164:	gap of 100 bp
*	69065	101518:	contig of 32354 bp in length
*	101519	101618:	gap of 100 bp
*	101619	114344:	contig of 12736 bp in length

FEATURES

```

Location/Qualifiers
1. .114344
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/clonename="RP13-97115"
/clone.lib="RPC1-13.1"
1. .13809
/note="assembly_fragment:00241"
fragment_chain:1
clone_end:SP6
vector_side:left"
13910. .51507
/note="assembly_fragment:00680"
fragment_chain:1"
51608. .65679
/note="assembly_fragment:00207"
fragment_chain:1"
65780. .69064
/note="assembly_fragment:00300"
69165. .101518
/note="assembly_fragment:01024"
101619. .114344
/note="assembly_fragment:01825"
clone_end:w7
vector_side:right"

```

BASE COUNT	32658 a	24338 c	24232 g	32616 t	500 others
ORIGIN					

[illegible]

repeat_region	3835..4145	/note="AluJb repeat: matches 1..310 of consensus"
repeat_region	4173..4486	/note="AluX repeat: matches 1..312 of consensus"
repeat_region	4482..5096	/note="MLT2 repeat: matches 1..119 of consensus"
repeat_region	5098..5254	/note="AluSg repeat: matches 2..162 of consensus"
repeat_region	5288..5529	/note="L2 repeat: matches 2429..2705 of consensus"
repeat_region	5597..5710	/note="MIR repeat: matches 32..151 of consensus"
repeat_region	6178..6471	/note="AluSg repeat: matches 1..296 of consensus"
repeat_region	7218..7504	/note="AluJo repeat: matches 2..302 of consensus"
repeat_region	7598..7692	/note="MIR repeat: matches 67..169 of consensus"
misc_feature	8791..9673	/note="CPG island"
repeat_region	9015..9136	/evidence=not_experimental
repeat_region	9677..9718	/note="61 copies 2 mer ct 69% conserved"
repeat_region	9745..10036	/note="21 copies 2 mer tt 85% conserved"
repeat_region	10351..10751	/note="MER92c repeat: matches 272..552 of consensus"
repeat_region	10857..10969	/note="MIR repeat: matches 40..154 of consensus"
repeat_region	11521..11613	/note="MIR repeat: matches 63..156 of consensus"
repeat_region	11829..12187	/note="L2 repeat: matches 1779..2341 of consensus"
repeat_region	12438..12548	/note="L1MA9 repeat: matches 6163..6270 of consensus"
repeat_region	12975..13093	/note="MIR repeat: matches 98..247 of consensus"
repeat_region	14083..14381	/note="AluX repeat: matches 1..293 of consensus"
repeat_region	14906..15126	/note="L2 repeat: matches 2364..2569 of consensus"
repeat_region	15142..15370	/note="MER4B repeat: matches 1..215 of consensus"
repeat_region	15366..16028	/note="MER4D repeat: matches 359..1017 of consensus"
repeat_region	16097..16211	/note="L2 repeat: matches 2631..2749 of consensus"
repeat_region	16199..16240	/note="L2 repeat: matches 2560..2599 of consensus"
repeat_region	18264..18349	/note="43 copies 2 mer ga 62% conserved"
repeat_region	19489..19797	/note="AluJb repeat: matches 1..306 of consensus"
repeat_region	19826..20044	/note="L1M3 repeat: matches 5220..5419 of consensus"
repeat_region	20045..20175	/note="FLAN_A repeat: matches 1..131 of consensus"
repeat_region	20176..20249	/note="L1M3 repeat: matches 5419..5496 of consensus"
repeat_region	20270..20929	/note="L1MA5A repeat: matches 5447..6104 of consensus"
repeat_region	20930..21226	/note="AluSx repeat: matches 1..297 of consensus"
repeat_region	21227..21417	/note="L1MA5A repeat: matches 6104..6294 of consensus"
repeat_region	21418..21461	/note="L1MA repeat: matches 4295..4338 of consensus"
repeat_region	21500..23928	/note="L1PA5 repeat: matches 3696..6143 of consensus"
repeat_region	24145..24341	/note="L1MEC repeat: matches 1820..2012 of consensus"

repeat_region	24385..24681 /note="AluX repeat: matches 1..296 of consensus"
repeat_region	24718..28764 /note="L1PA4 repeat: matches 2108..6144 of consensus"
repeat_region	28765..28886 /note="FLAM_C repeat: matches 3..124 of consensus"
repeat_region	28894..28928 /note="L1PA4 repeat: matches 2064..2097 of consensus"
repeat_region	28929..29221 /note="AluSc repeat: matches 1..296 of consensus"
repeat_region	29222..29377 /note="L1MEC repeat: matches 2097..2258 of consensus"
repeat_region	29428..29551 /note="L2 repeat: matches 2621..2749 of consensus"
repeat_region	29553..29644 /note="Aluub repeat: matches 205..296 of consensus"
repeat_region	29648..30097 /note="MER87 repeat: matches 1..469 of consensus"
repeat_region	30104..30153 /note="25 copies 2 mer ca 76% conserved"
repeat_region	31811..31976 /note="MIR repeat: matches 46..204 of consensus"
repeat_region	32005..32260 /note="128 copies 2 mer ta 80% conserved"
repeat_region	32903..33194 /note="AluJo repeat: matches 1..293 of consensus"
repeat_region	33677..34221 /note="MER68A repeat: matches 1..568 of consensus"
repeat_region	34372..35093 /note="TIGER1 repeat: matches 1650..2308 of consensus"
repeat_region	35094..35333 /note="L1PB1 repeat: matches 5909..6155 of consensus"
repeat_region	35334..35437 /note="TIGER1 repeat: matches 2308..2418 of consensus"
repeat_region	35477..35878 /note="MLT1-INTERNAL repeat: matches 923..1579 of consensus"
repeat_region	36082..36740 /note="MLT1-INTERNAL repeat: matches 201..885 of consensus"
repeat_region	36783..37121 /note="L2 repeat: matches 824..1219 of consensus"
repeat_region	37158..37328 /note="L1M4 repeat: matches 4640..4816 of consensus"
repeat_region	39953..39978 /note="13 copies 2 mer ca 100% conserved"
repeat_region	40525..40566 /note="MIR repeat: matches 110..151 of consensus"
repeat_region	44063..44377 /note="AluJo repeat: matches 1..299 of consensus"
repeat_region	44451..45182 /note="MER21B repeat: matches 3..790 of consensus"
repeat_region	45243..45477 /note="L1M4 repeat: matches 4078..4321 of consensus"
repeat_region	45515..45890 /note="L1PA7 repeat: matches 5769..6143 of consensus"
repeat_region	45900..47783 /note="L1PA8 repeat: matches 4284..6161 of consensus"
repeat_region	47776..48115 /note="L1M4 repeat: matches 3680..4029 of consensus"
repeat_region	48116..48477 /note="MER47A repeat: matches 1..365 of consensus"
repeat_region	48478..48554

	Query Match	21.5%	Score 167.8	DB 9	Length 149749
	Best Local Similarity	70.8%	Pred. No. 4.4e-35		
	Matches 288	Conservative	97	Indels 22	Gaps 4
Qy	10	CTGTGAGCGCGGACTCGGGTCCCTTGAGTCTGTGAGATCTTCTCCGCTACTGAGACACGG	69		
Db	76290	CTTGAGCTGTGAGGCCAAGTCTTCAAGCTGTAGATCTTCTTCCTACTGAGATGCAG	76349		
Qy	70	CGGCTAGGTCCACAGCGCAGATCCAACTCGGAGTCTCAAGTGTGAGTGTGAGAGGAA	129		

Db 76350 CAGGTAGTCCACAGGCCAATCCAACTGGGAGTTGAAGTGTGACTGAGGTGAGGAGGAG 76409
Qy 130 CCAGCAGGCTCCCGCAGGGT---TCTGTGTCTCACTGACTCAGACTGAGAAGGCCCTCGAA 186
Db 76410 CCAGTGGCTCTCGAGGGTCAACGGTGGGAGGAGACTCAGAGGAGAGAGGCCCTCGAG 76469
Qy 187 GTCGTGCGTCCCTCTCATGCGGTGTCACGCCCATGAGCTTCTTCTGTCACGGCCATA 246
Db 76470 GTCCTTCATCTCTTATATGTCGACTGCGACCATGGGCTTCTT-TTTTGTGGGGCCACA 76528
Qy 247 ACTAGGAGGAGGAGGCCGAGCAGTGGAGGCTCAGGGCCTAGGGCAAGCTGGGT----- 298
Db 76529 ACTGGGAGGAGGAGGGCTCGGCATGGGGGAGCTGGGTATGATGGGTGCATCTG 76588
Qy 299 -----GCTGTGTTGGGGTATCCGATCCAGAGCACCTGGAAACCC-----GACAGAAGA 348
Db 76589 GGGGAGCTGTGGAGGTATCTGATCCCAAGAAATGCCTCAAGCCGCCCAAAAGAGGACAGA 76648
Qy 349 TTCTGGACTCCCGACGGGACCGAGGAGGAGGCGGATGAGCGACA 395
Db 76649 TTGTAGACTCCCGAGGGGGACCGAGGAGGCGGCTGGGTGGCA 76695

RESULT 29
AL590240 Human DNA sequence from clone RPl1-26613 on chromosome X, complete
sequence.
ACCESSION AL590240 AC025380
VERSION AL590240.5 GI:13872461
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 130005)
Clark.S.
Direct Submission
Submitted (25-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On May 15, 2001 this sequence version replaced gi:8705130
gi:13785125.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30);
an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/ChrX>
RPl1-26613 is from the library RPl1-11.1 constructed by the group
of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
RPl1-26613 it may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.

The true left end of clone RPl1-382F24 is at 129906 in this
sequence. The true right end of clone RPl1-296K21 is at 100 in this
sequence.

FEATURES source

Location/Qualifiers

1..130005
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RPl1-26613"
/clone_lib="RPl1-11.1"
1..3875
/note="Lip repeat: matches 4..3892 of consensus"
repeat_region
4031..4472
/note="LIP repeat: matches 5718..6165 of consensus"
repeat_region
4477..4658
/note="LIME3A repeat: matches 5967..6157 of consensus"
repeat_region
4869..5170
/note="AluSc repeat: matches 1..306 of consensus"
repeat_region
6010..6307
/note="AluSx repeat: matches 1..299 of consensus"
repeat_region
9580..9670
/note="MIR repeat: matches 127..214 of consensus"
repeat_region
10019..10387
/note="MLT1B repeat: matches 41..390 of consensus"
repeat_region
10424..11726
/note="LIM47 repeat: matches 4980..6284 of consensus"
repeat_region
12183..12372
/note="LIP repeat: matches 5963..6153 of consensus"
repeat_region
12387..17012
/note="LIME2 repeat: matches 1626..6308 of consensus"
repeat_region
17013..17325
/note="AluSg repeat: matches 1..313 of consensus"
repeat_region
17326..17971
/note="LIM42 repeat: matches 979..1626 of consensus"
repeat_region
18003..24449
/note="LIP repeat: matches 6..6143 of consensus"
repeat_region
24463..24926
/note="LIP repeat: matches 4190..4658 of consensus"
repeat_region
25188..25377
/note="LIM4 repeat: matches 4619..4820 of consensus"
repeat_region
27242..27405
/note="82 copies 2 mer ta 76% conserved"
repeat_region
27731..27937
/note="LIM4 repeat: matches 2..231 of consensus"
repeat_region
28628..28710
/note="AluJ/FLAM repeat: matches 2..84 of consensus"
repeat_region
28760..28926
/note="LIM48 repeat: matches 6114..6290 of consensus"
repeat_region
30040..30466
/note="LIR9 repeat: matches 198..625 of consensus"
repeat_region
30467..31208
/note="L1 repeat: matches 3291..4031 of consensus"
repeat_region
31209..31480
/note="AluSx repeat: matches 38..311 of consensus"
repeat_region
31481..32418
/note="L1 repeat: matches 2350..3291 of consensus"
repeat_region
32439..33203
/note="LIP repeat: matches 5395..6144 of consensus"
repeat_region
33211..33753
/note="LIP repeat: matches 1840..2380 of consensus"
repeat_region
33748..35989
/note="LIP repeat: matches 2006..4258 of consensus"
repeat_region
35992..36686
/note="LIP repeat: matches 5449..6146 of consensus"
repeat_region
36689..37628
/note="20 copies 2 mer aa 80% conserved"
repeat_region
36730..37022
/note="LIP repeat: matches 1564..1858 of consensus"
repeat_region
37018..37317
/note="LIP repeat: matches 5312..5604 of consensus"
repeat_region
37327..37629
/note="AluSx repeat: matches 1..303 of consensus"
repeat_region
37630..37763

closure of gap impossible.
The true right end of clone L21F12 is at 10842 in this sequence.
The true left end of clone L185E6 is at 1 in this sequence. L185E6
is from cosmid library LA04NC01 constructed at the Human Genome
Center, Los Alamos National Laboratory, NM 87545 under the auspices
of the U.S. Department of Energy. The library was constructed using
flow-sorted human chromosome 4 from a Hamster-Human hybrid cell
line (UV20HL21-27) containing human chromosomes 4, 8 and 21.
VECTOR: scos1
L185E6 is contained in a clone contig spanning
2Mb which is described in Baxendale et al, Nature Genetics 4 (1993
) 181- 186. See also Myers et al, Cytogenet Cell Genet. 66 (1994
) 218-230.

```
FEATURES
Source
1..20587
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4p16.3"
/clone_lib="LA04NC01"
/cell_line="UV20HL21-27"
/clone="LA04NC01-185E6"
/complement(1370..1739)
/note="match: STS L00885"
2380..4066
/note="L1 element fragment"
4115..4400
/note="Alu repeat: matches 1..308 of consensus"
4427..4736
/note="L1 element fragment"
4778..5099
/note="L1 element fragment"
5203..5333
/note="MSTC element fragment"
5632..5721
/note="L1 element fragment"
5980..6714
/note="matches Trk-2h oncogene - 41aa of human RL7A_HUMAN
M36072"
/codon_start=1
/pseudo
6747..6778
/note="16 copies of 2 mer 100 % conserved"
10906..11082
/partial
/note="Alu repeat: matches 1..191 of consensus"
11083..11214
/partial
/note="Alu repeat: matches 175..308 of consensus"
11352..11506
/partial
/note="Alu repeat: matches 308..351 of consensus"
13249..13799
/note="putative CpG island"
15946..16238
/note="Alu repeat: matches 1..308 of consensus"
17069..17143
/note="MT1D element fragment"
17589..17689
/partial
/note="Alu repeat: matches 308..210 of consensus"
17695..17739
/partial
/note="Alu repeat: matches 170..114 of consensus"
18268..18369
/partial
/note="Alu repeat: matches 155..38 of consensus"
19668..19742
/note="MIR element fragment"
20313..20524
/note="4 copies of 53 mer 83 % conserved"
5439 a 5367 c 4601 g 5180 t
BASE COUNT
ORIGIN
```

```
Query Match      21.0%; Score 164.2; DB 9; Length 20587;
Best Local Similarity 75.1%; Pred. No. 3.9e-34;
Matches 247; Conservative 0; Mismatches 73; Indels 9; Gaps 3;

Oy 429 GAGCCCACTAATGGAGAGCCCAAAAAGCAAGACAGCAGCTGAAAGTCGGGATCCTACA 488
      ||||| || || || || || || || || || || || || || || || || || || ||
Db 18056 GAGCCCACTGATGAGCACCCTCAGCAAGAGGACACCACCTGAAAGTCGGGCTTT--A 17999

Oy 489 CCTGGGAGCAGACAGAGAAGATCAGGTACAGTCCAGTCCAGTCCGCGACATGAA 548
      ||||| || || || || || || || || || || || || || || || || || || ||
Db 17998 CTTGCCAGGAGAGAGGAAGATCACGGTGTCTGTAGATTCTGTGCTTGCACAGGAA 17939

Oy 549 GGTGATCTGAAGAGCTGCATCAGTCAACACCGGGGATAAATCTGGATTGGGTTCGG 608
      ||||| || || || || || || || || || || || || || || || || || || ||
Db 17938 GCTGATCTCCGGGAGCTGCTCTC----AAAGACTGGGATGAATGTGGAGATGG--TCCTG 17886

Oy 609 CGTCAAGGTGAAGATAATACCTTAAGAGGAACTGTAAAAATGCCAGAGCGTGAAGA 668
      || || || || || || || || || || || || || || || || || || || || ||
Db 17885 ATGTCGGGGAATATTCTGCCGCAATCAGAGCAATTTAAATTGCCAGAAGAGGTGAAG 17826

Oy 669 GCACCAACAAGTTTAAATGAAGACAAGCTGAACAACGCCAAGCTGTTTATATTAGATA 728
      ||||| || || || || || || || || || || || || || || || || || || ||
Db 17825 GCAACCCACAGGTTCCAGGAGAGACAAGCTGAACAATGCAAACTGGTTTATATTAGATA 17766

Oy 729 TTTGACTTAAACTATCTCAATAAAGTTTT 757
      ||||| || || || || || || || || || || || || || || || || || || ||
Db 17765 CGTGACTTAAATAATCTCAATACAGTTTT 17737

RESULT 31
HS193G15/c
LOCUS
DEFINITION
Human DNA sequence from clone 193G15 on chromosome 4. Contains the
5' part of the RGS12 gene for regulator of G-protein signalling 12,
an RPL7A (60S Ribosomal Protein 7A (SURF3)) pseudogene, ESTs, an
STS, GSSS and a putative CpG island, complete sequence.
ACCESSION
AL117391
VERSION
AL117391.1 Gi:5911814
KEYWORDS
HTG; 60S Ribosomal Protein 7A; CpG Island; G-protein; RGS12; RPL7A;
SURF3.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 62493)
AUTHORS
McMurray,A.
TITLE
Direct Submission
JOURNAL
Submitted (28-JUN-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Enr., EMBL; Swi., SWISSPROT; Tr., TREMBL
IMPORTANT: This sequence is not the entire insert of clone 193G15.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
The true left end of clone 1E6 (L21F12) is at 6371 in this
sequence. The true right end of clone 361H4 is at 104 in this
sequence. This sequence has been finished according to sequencing
criteria as follows. An attempt is made to resolve all sequencing
problems, such as compressions and repeats, but not necessarily
within known annotated human repeat sequence elements (e.g. Alu).
Where the sequence is ambiguous, there is an annotation using the
'unsure' feature key.
This sequence was generated from part of bacterial clone contigs of
```

human chromosome 4, constructed by the Sanger Centre Human Genetics Group.
193G15 is from the library RPC11 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/VECTOR:PCYPAC2>.

FEATURES

source

Location/Qualifiers

1. .62493

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="4"

/clone="193G15"

/clone_lib="RPC11"

677. .786

/note="L2 repeat: matches 2598. .2704 of consensus"

1326. .1493

/note="MER58A repeat: matches 1. .204 of consensus"

3474. .4043

/note="15 copies 38 mer 68% conserved"

3481. .4074

/note="9 copies 66 mer 69% conserved"

3485. .4056

/note="286 copies 2 mer ca 69% conserved"

3485. .4034

/note="11 copies 50 mer 70% conserved"

4004. .4268

/note="5 copies 53 mer 69% conserved"

4015. .4210

/note="4 copies 49 mer 75% conserved"

4059. .4230

/note="86 copies 2 mer ac 65% conserved"

4240. .4353

/note="3 copies 38 mer 76% conserved"

5459. .5717

/note="L1M3 repeat: matches 5669. .5949 of consensus"

5774. .5834

/note="L1M4 repeat: matches 5296. .5356 of consensus"

6069. .6611

/note="L1M3 repeat: matches 2916. .3552 of consensus"

6612. .6734

/note="AluJb repeat: matches 2. .125 of consensus"

6735. .6747

/note="L1M3 repeat: matches 3552. .3566 of consensus"

6748. .7059

/note="AluX repeat: matches 1. .312 of consensus"

7060. .7230

/note="L1M3 repeat: matches 3566. .3618 of consensus"

7220. .7813

/note="9 copies 66 mer 68% conserved"

7225. .7794

/note="15 copies 38 mer 67% conserved"

7231. .7806

/note="288 copies 2 mer gg 67% conserved"

7249. .7787

/note="11 copies 49 mer 69% conserved"

7250. .7799

/note="11 copies 50 mer 68% conserved"

7271. .7800

/note="10 copies 53 mer 68% conserved"

7816. .10309

/note="L1M3 repeat: matches 3611. .6184 of consensus"

9731. .9733

/note="clone IE6

act in this entry

substitution"

/replace="att"

10316. .10627

/note="AluJb repeat: matches 1. .308 of consensus"

10618. .10620

/note="clone IE6

act in this entry

insertion"

/replace="at"

10640. .10734

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

variation

variation

repeat_region

repeat_region

repeat_region

repeat_region

variation

variation

repeat_region

variation

repeat_region

repeat_region

repeat_region

variation

repeat_region

variation

repeat_region

/note="L1M4 repeat: matches 4567. .4667 of consensus"
10738. .10845
/note="L1 repeat: matches 4239. .4341 of consensus"
10846. .11150
/note="AluJb repeat: matches 8. .312 of consensus"
11151. .11763
/note="L1 repeat: matches 3588. .4239 of consensus"
11741. .12214
/note="L1M4 repeat: matches 2684. .3192 of consensus"
12693. .13778
/note="HERV16 repeat: matches 1851. .2990 of consensus"
12858. .12860
/note="clone IE6
ggg in this entry
substitution"
/replace="gag"
13361. .13363
/note="clone IE6
atg in this entry
substitution"
/replace="acg"
13779. .14217
/note="MER65A repeat: matches 1. .445 of consensus"
14300. .15958
/note="MER65-internal repeat: matches 81. .1984 of
consensus"
15959. .16270
/note="AluJo repeat: matches 1. .312 of consensus"
16271. .16821
/note="MER65-internal repeat: matches 1984. .2522 of
consensus"
16467. .16469
/note="clone IE6
aac in this entry
substitution"
/replace="agc"
16691. .16693
/note="clone IE6
cat in this entry
substitution"
/replace="cgt"
17094. .17636
/note="MER4-internal repeat: matches 2942. .3475 of
consensus"
17123. .17126
/note="clone IE6
gagt in this entry
insertion"
/replace="gt"
17835. .18059
/note="MER4-internal repeat: matches 3494. .3730 of
consensus"
17886. .18314
/note="MER83-internal repeat: matches 2896. .3312 of
consensus"
18140. .19206
/note="MER65-internal repeat: matches 2477. .3523 of
consensus"
18148. .18150
/note="clone IE6
ata in this entry
substitution"
/replace="aca"
19207. .19507
/note="AluY repeat: matches 1. .301 of consensus"
19304. .19306
/note="clone IE6
gat in this entry
substitution"
/replace="gtt"
19508. .20629
/note="MER65-internal repeat: matches 3523. .4351 of
consensus"

Db 98160 GCACACAGGTTCCAGGACACAGCTGAACAATGCAAACTGGTTTATATTAGATA 98101

Qy 729 TTGACTTAACACTACTCTCAATAAGTTT 757

Db 98100 CGTGACTTAAATATCTCAATACAGTTT 98072

RESULT 34

AX198429

LOCUS

DEFINITION

Sequence 884 from Patent WO0151513.

AX198429

ACCESSION

VERSION

AX198429.1 GI:15388750

KEYWORDS

human.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 320)

Algate,P.A.

Ovarian tumor-associated sequences

PATENT: WO 0151513-A 884 19-JUL-2001;

CORIXA CORPORATION (US)

FEATURES

Source

Location/Qualifiers

1..320

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT

96 a 65 c 85 g 74 t

ORIGIN

Query Match 17.3%; Score 135; DB 6; Length 320;

Best Local Similarity 79.0%; Pred. No. 3.4e-26;

Matches 173; Conservative 0; Mismatches 45; Indels 1; Gaps 1;

Qy 523 CTGAGATCCAGTCCGCGACATGTCGAAGGTGATCTGCAAGAGCTGCATCAGTCAAAACACCG 582

Db 1 CTGAGATTCAAGTGCCTGACCTGGAAGCGGATCTCCAGGAGCTATGTCAGACAAAGACTG 60

Qy 583 GGGATAAATCTGGATTTCGGGTTCCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACAC 642

Db 61 GGGATGGATGTGAAGT-GGTACTGATGTCGAAGGGGAAGATTCTACCAAAAGCAGAGCAC 119

Qy 643 TGTAATAATCCAGACAGCTGAAGACCAACCAAGTTTAAATCAACACAGCTGAAC 702

Db 120 TTTAAATGCCAGAGCAGGTGAAGGAAATCACAGGTTTAAAGGAAGATAAGCTGAAC 179

Qy 703 AACCAAGCTGGTTTATATTAGATATTGACTT 736

Db 180 AACACAACTGTTTATATTAGATATTTACTT 213

RESULT 35

AX208978

LOCUS

DEFINITION

Sequence 818 from Patent WO0157207.

AX208978

ACCESSION

VERSION

AX208978.1 GI:15423401

KEYWORDS

human.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 214)

Algate,P.A. and Mannion,J.

Compositions and methods for the therapy and diagnosis of ovarian cancer

PATENT: WO 0157207-A 818 09-AUG-2001;

CORIXA CORPORATION (US)

FEATURES

Source

Location/Qualifiers

1..214

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT

74 a 34 c 55 g 51 t

ORIGIN

Query Match 17.1%; Score 133.2; DB 6; Length 214;

Best Local Similarity 79.4%; Pred. No. 1e-25;

Matches 170; Conservative 0; Mismatches 43; Indels 1; Gaps 1;

Qy 523 CTGAGATCCAGTCCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCAGTCAAAACACCG 582

Db 1 CTGAGATTCAAGTGCCTGACCTGGAAGCGGATCTCCAGGAGCTATGTCAGACAAAGACTG 60

Qy 583 GGGATAAATCTGGATTTCGGGTTCCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACAC 642

Db 61 GGGATGGATGTGAAGT-GGTACTGATGTCGAAGGGGAAGATTCTACCAAAAGCAGAGCAC 119

Qy 643 TGTAATAATCCAGACAGCTGAAGACCAACCAAGTTTAAATCAACACAGCTGAAC 702

Db 120 TTTAAATGCCAGAGCAGGTGAAGGAAATCACAGGTTTAAAGGAAGATAAGCTGAAC 179

Qy 703 AACCAAGCTGGTTTATATTAGATATTGACTT 736

Db 180 AACACAACTGTTTATATTAGATATTTACTT 213

RESULT 36

AC090022

LOCUS

DEFINITION

Homo sapiens chromosome 12q clone rePl1-154D9, WORKING DRAFT

SEQUENCE, 4 unordered pieces.

AC090022

ACCESSION

AC090022.9 GI:14547672

KEYWORDS

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 164591)

Mu-y,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbara,J.,

Benton,J., Blimege,K., Blankenburg,K., Bonnin,D., Bouck,J.,

Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,

Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,

Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,

Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.B., Cox,C.,

Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,

Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,

Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Edgar,D., Edwards,C.C.,

Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,

Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,

Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,

Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,

Hamilton,K., Harris,C., Harris,K., Hart,M., Haviak,P., Hawes,A.,

Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,

Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,

Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,

Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,

Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,

Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,

Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,

Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,

Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,

Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,

Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,

Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S.,

Ogulu,M., Okuwonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,

Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,

Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojebokan,I., Rolfe,M.,

Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,

Sisson,I., Sodergren,E., Sonaie,T., Sparks,A., Stanley,H.,

Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,

Tang,H., Tansey,J., Taylor,C., Taylor,F., Telford,B., Thomas,N.,

Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,

Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,

Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,

using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor. For further details, see <http://bacpac.med.buffalo.edu/>. The clone is available from Genome Systems, Inc. (<http://www.genomesystems.com>).

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP5-848B16, 200 bp overlap. Actual start of this clone is at base position 1 of RP4-698G21; actual end is 109273 of RP4-698G21.

This clone contains STS SWSS3337 (NID:g1113739).

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="7"

/map="p21-p22"

/clone="RP4-698G21"

/clone_lib="RPC1-4"

386..420

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474..567

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586..962

/rpt_family="MaLR"

968..1041

/rpt_family="L2"

1045..1109

/rpt_family="MaLR"

1157..1410

/rpt_family="L2"

3108..3194

/rpt_family="MIR"

4869..11012

/rpt_family="L1"

11296..11387

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11395..11702

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12129..12213

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14481..14668

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18027..18324

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21120..21421

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24376..24504

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24514..24578

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25630..26169

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27828..28703

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29740..30022

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34660..34976

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35070..35203

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39132..39429
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41307..41600
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44883..45881
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49179..49480
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50097..50184
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52842..52897
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53288..53667
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54194..54584
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57119..57245
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57390..57660
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57742..57865
/rpt_family="MIR"
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/note="match to EST AA551305 (NID:g2321557) nk71b08.s1"
58589..58850
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60889..61048
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62270..62322
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62528..63508
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63703..69828
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69839..75304
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76788..76902
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77385..77693
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78108..78287
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78771..79368
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79740..79832
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82376..82765
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83415..83536
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85229..85584
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86335..86595
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86927..87104
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88291..88397
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88394..88507
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88539..88650
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90033..90339

Query Match

Best Local Similarity 14.5%; Score 113.4; DB 9; Length 109469;
63.6%; Pred. No. 4.1e-20;

Matches 260; Conservative 0; Mismatches 131; Indels 18; Gaps 5;

Qy 1 CGCGCGAGCTGTGAGCCGCGA--CTCGGGTCCCTGAGCTGTGATTTCTCCGCTA 58
|||||
Db 36964 CGCGCGAGCTGTGAGGCTGTGAGGTCGCGCTCTCTCTCTGGACTTTTCTGTCTA 37023

Qy 59 CTGAGACACGCGGTAGTCCACAGCAGATCAACTGGGAGTTGAAGTGTGAGTGAGA 118
|||||
Db 37024 CTGAGACACGCGGTAGTCCGAGGCCAGTCTTCCAGGGGTTGAAGTGTGAGTGAGT 37083

Qy 119 GTGAAGAGGAACACGAGGTTCCGGAGGTTGTG-----TGTCTAGTGACTCAGAGTG 172
|||||
Db 37084 GTGAGGAGGACCCAGCGCGTCTGGAGCATGGGCGAGCTGTGCGCTCGAGGCG 37143

Qy 173 AGAAGCCCTCGAAGTCTGCTCCTCTCTATGCGGTGCCAGCCCATGGACCTTCTTCTC 232
|||||
Db 37144 CGATGGGTCTCAAGTGATCGTCTCTCTCGTGAAGTGGCAGCCGATGGGCTTTGTT 37203

Qy 233 TCGTCACGGCCATAACTAGGAGGAAGAGGGCCGAGGAGTGGAG-GGGCTCAGGCGAAG 291
|||||
Db 37204 GTAGTGGGTGAGAACGAGGAGGTGGGCGCGTGTGAGAGGCTCAGTGAAG 37263

Qy 292 CTGGG----GTGCTGTGGGGGTATCCGAGTCCAGAGCACCTGGAAACC-----CCGAC 342
|||||
Db 37264 ATGGGGTAAGTCTCTGGGGTCTGAGCAGGTATCGGAGTCCGTGGAAACCTCGACAGAG 37323

Qy 343 AGAAGATTCTGGACTCCCGACAGCGGACGAGGAGGCGGATGAGC 391
|||||
Db 37324 GACAGATTCTGGACTCTCTCGCGAGCCAGGAGGCGGGTGGCG 37372

RESULT 38
AF055473
LOCUS Homo sapiens GAGE-8 mRNA, complete cds. PRI 01-MAY-2000
DEFINITION AF055473
ACCESSION AF055473
VERSION AF055473.1 GI:3511022
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 528)
De Backer,O., Arden,K.C., Boretti,M., Vantomme,V., De Smet,C.,
Czekay,S., Viars,C.S., De Plaen,E., Brasseur,F., Chomez,P., Van den
Eynde,B., Boon,T. and van der Bruggen,P.
Characterization of the GAGE genes that are expressed in various
human cancers and in normal testis
Cancer Res. 59 (13), 3157-3165 (1999)
JOURNAL 99323388
MEDLINE 10397259
PUBMED
REFERENCE 2 (bases 1 to 528)
De Backer,O.R.Y.
Direct Submission
TITLE Submitted (24-MAR-1998) Ludwig Institute for Cancer Research,
JOURNAL Brussels Branch, 74 av. Hippocrate, Brussels B-1200, Belgium
FEATURES
source
1..528
/organism="Homo sapiens"
/db_xref="taxon:9606"
73..423
CDS
/codon_start=1
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/protein_id="AAC33676.1"
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BASE COUNT 158 a 112 c 151 g 107 t

Query Match 14.1%; Score 110; DB 9; Length 528;
Best Local Similarity 63.9%; Pred. No. 2.6e-19;

Matches 216; Conservative 0; Mismatches 115; Indels 7; Gaps 3;

Qy 447 CCCCCAAAAGAACACACGAGCTGAAAGTCGGATCCTACACCTGGCGAGCAGACAGAA 506
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Db 190 CTTGAAGAAGGGGAACGACCAACTCAACGTCAAGATCTGCTGAGGAG---GGA 246

Qy 507 GAAGATTCAAGTACAGCTGAGATCCCAAGTCGCGACATGGAAGTGTGATCTGCAAGAGCTG 566
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Db 247 GAGGATGAGGGAGCATCTGAGGTCAAGGCCCAAGCCTGAAGCTGATAGCCAGGAACAG 306

Qy 567 CATCAGTCAAAACACCGGGGATAAATCTGGATTTGGGTTCGGCGTCAAGGTGAAGATAAT 626
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Db 307 GGTCAACCCACAGACTGGGTGTGAGTGTGAAGAT-GGTCTGTATGGCGCAGCATGGACCC 365

Qy 627 ACCTAAGAGGAGACACTGTAAATGCCAAGACGAGTGAAGACCAACCAACCTTTAAAT 686
|||||
Db 366 GCCAAATCCAGAGGAGTGAACAGCCTGAAGAAGGTGAACAATCACAGTGTTAATA 425

Qy 687 GAAGACAAGTGAACACAGCAGCTGGTTTATATATAGATATTTG---ACTTAAACTAT 743
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Db 426 GAAGACAGTTGAATATGATGACGGCTGCTCTATGTTGAAATTTGTTCAATAATTTCT 485

Qy 744 CTCAATAAGTTTTCGAGCTTTTCAACCAAAAAA 781
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Db 486 CCCAATAAGCTTTACAGGCTTCTGCAAGAAAAA 523

RESULT 39
AR028492
LOCUS Sequence 18 from patent US 5858689.
DEFINITION AR028492
ACCESSION AR028492
VERSION AR028492.1 GI:5940465
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 539)
van der Bruggen,P., van den Eynde,B., DeBacker,O. and
Boon-Failleur,T.
Isolated peptides derived from the gage tumor rejection antigen
precursor and uses thereof
Patent: US 5858689-A 18 12-JAN-1999;
JOURNAL Location/Qualifiers
FEATURES
source
1..539
/organism="unknown"
BASE COUNT 158 a 113 c 157 g 111 t
ORIGIN
Query Match 14.1%; Score 110; DB 6; Length 539;
Best Local Similarity 63.9%; Pred. No. 2.6e-19;
Matches 216; Conservative 0; Mismatches 115; Indels 7; Gaps 3;

Qy 447 CCCCCAAAAGAACACACGAGCTGAAAGTCGGATCCTACACCTGGCGAGCAGACAGAA 506
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Db 202 CCTGAAGAAGGGGAACCCAGCAACTCAACGTCAAGATCTGCTGAGGAG---GGA 258

Qy 507 GAAGATCAGGATACAGCTGAGATCCCAAGTCGCGACATGGAAGTGTGATCTGCAAGAGCTG 566
|||||
Db 259 GAGGATGAGGAGGATCTGCAAGGTCAAGGCCGAAGCCTGAAGCTGATAGCCAGGAACAG 318

Qy 567 CATCAGTCAAAACACCGGGGATAAATCTGGATTTGGGTTCGGCGTCAAGGTGAAGATAAT 626
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Db 319 GGTCACCCACAGACTGGGTGTGAGTGTGAAGAT-GGTCTGTATGGCGAGGAGTGGACCC 377

Qy 627 ACCTAAGAGAGAACACTGTAAATGCCAAGACGAGTGAAGACCAACCAACCTTTAAAT 686
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Db 378 GCCAAATCCAGAGGAGTGAACAGCCTGAAGAAGGTGAACAATCACAGTGTTAATA 437

Qy 687 GAAGACAAGCTGAACCAACCAACGCTGTTTATATATAGATATTTG---ACTTAAACTAT 743
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Db 438 GAAGACAGTTGAATATGATGACGGCTGCTCTATGTTGGAATTTGTTCAATAATTTCT 497

Thu Oct 17 09:19:16 2002

c 83	18	2.3	1396	22	AAH17151	Human cDNA sequenc	c 156	17	2.2	474	22	AAK62159	Human immune/haema
c 84	18	2.3	1471	22	AAI59131	Human polynucleoti	c 157	17	2.2	475	22	ABA25109	Probe #3575 for qe
c 85	18	2.3	1572	22	AAF27283	Human atonal homol	c 158	17	2.2	475	22	AAK03627	Human brain expres
c 86	18	2.3	1832	21	AAC36377	Arabidopsis thalia	c 159	17	2.2	475	22	AAK29086	Human bone marrow
c 87	18	2.3	1836	21	AAC50584	Arabidopsis thalia	c 160	17	2.2	475	22	AAI03552	Probe #3543 used t
c 88	18	2.3	1853	21	AAAT78405	Human secreted pro	c 161	17	2.2	536	22	AAH10605	Human cDNA clone (
c 89	18	2.3	1897	18	AAAT71258	Human secreted pro	c 162	17	2.2	590	22	AAH34745	Human colon cancer
c 90	18	2.3	1897	18	AAZ60821	Proviral oncogene	c 163	17	2.2	612	20	AAZ24864	Human secreted pro
c 91	18	2.3	1967	22	AAAS00836	Nucleotide sequenc	c 164	17	2.2	620	21	AAZ54242	Arabidopsis thalia
c 92	18	2.3	2394	22	AAAC85095	Human cDNA clone H	c 165	17	2.2	684	21	AAAC43832	Arabidopsis thalia
c 93	18	2.3	2714	23	ABL22182	Atherosclerosis-as	c 166	17	2.2	708	20	AAI18952	Partial human PI3K
c 94	18	2.3	3261	20	AAV64855	Drosophila melanog	c 167	17	2.2	708	21	AAI18952	Arabidopsis thalia
c 95	18	2.3	3410	22	AAK53375	Human LFA-1 alpha	c 168	17	2.2	709	21	AAAC54365	Arabidopsis thalia
c 96	18	2.3	3510	22	AAAT7651	Human polynucleoti	c 169	17	2.2	731	21	AAAC53473	Arabidopsis thalia
c 97	18	2.3	3585	17	AAAT7651	Human LFA-1 alpha	c 170	17	2.2	731	21	AAAC43954	Human pax protein
c 98	18	2.3	3650	23	AAAF6684	Human LFA-1 alpha	c 171	17	2.2	744	24	AAI71487	Human validated ca
c 99	18	2.3	4980	22	AAAF6684	Human LFA-1 alpha	c 172	17	2.2	752	20	AAAX98945	Human validated ca
c 100	18	2.3	5133	21	AAAF6684	Human LFA-1 alpha	c 173	17	2.2	759	20	AAAX98945	Human validated ca
c 101	18	2.3	5133	21	AAAF6684	Human LFA-1 alpha	c 174	17	2.2	763	22	AAI96392	Human neuroblastom
c 102	18	2.3	5133	21	AAAF6684	Human LFA-1 alpha	c 175	17	2.2	777	20	AAAX90046	Human validated ca
c 103	18	2.3	5133	21	AAAF6684	Human LFA-1 alpha	c 176	17	2.2	789	20	AAAX08693	Novel nucleotide s
c 104	18	2.3	5133	21	AAAF6684	Human LFA-1 alpha	c 177	17	2.2	789	20	AAAX08693	CPE 114 coding seq
c 105	18	2.3	5680	22	AAAF6684	Human LFA-1 alpha	c 178	17	2.2	794	21	AAH90810	Arabidopsis thalia
c 106	18	2.3	6012	24	AAAF6684	Human LFA-1 alpha	c 179	17	2.2	801	23	AAAS55745	Streptococcus pneu
c 107	18	2.3	6287	22	AAAF6684	Human LFA-1 alpha	c 180	17	2.2	801	23	AAAS55745	Streptococcus pneu
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c 110	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 183	17	2.2	813	22	AAH90915	B. subtilis panc g
c 111	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 184	17	2.2	813	22	AAH90915	DNA encoding novel
c 112	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 185	17	2.2	813	22	AAH90915	Gene No. 19 encodi
c 113	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 186	17	2.2	813	22	AAH90915	Genomic sequence #
c 114	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 187	17	2.2	813	22	AAH90915	Human immune/haema
c 115	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 188	17	2.2	813	22	AAH90915	Human digestive sy
c 116	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 189	17	2.2	813	22	AAH90915	Human leukocyte ce
c 117	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 190	17	2.2	813	22	AAH90915	Human diagnostic a
c 118	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 191	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 119	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 192	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 120	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 193	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 121	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 194	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 122	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 195	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 123	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 196	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 124	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 197	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 125	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 198	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 126	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 199	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 127	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 200	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 128	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 201	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 129	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 202	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 130	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 203	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 131	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 204	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 132	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 205	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 133	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 206	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 134	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 207	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 135	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 208	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 136	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 209	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 137	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 210	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 138	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 211	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 139	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 212	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 140	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 213	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 141	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 214	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 142	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 215	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 143	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 216	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 144	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 217	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 145	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 218	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 146	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 219	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 147	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 220	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 148	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 221	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 149	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 222	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 150	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 223	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 151	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 224	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 152	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 225	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 153	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 226	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 154	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 227	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ
c 155	18	2.3	7223	22	AAAF6684	Human LFA-1 alpha	c 228	17	2.2	813	22	AAH90915	Human PRO1565 (UNQ

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375	17	2.2	28818	22	AAL35901	Human musculoskele	c 448	16	2.0	255	22	AAH82245	Rat differential t
376	17	2.2	31056	22	AAL03450	Human reproductive	c 449	16	2.0	258	22	AAK57059	Human immune/haema
c 377	17	2.2	31969	23	ABL07768	Drosophila melanog	c 450	16	2.0	264	21	AAK87519	Rat hepatocyte car
378	17	2.2	32236	22	AAK91250	Human digestive sy	c 451	16	2.0	267	21	AAQ02146	Human secreted pro
379	17	2.2	36776	22	AAK86321	Human immune/haema	c 452	16	2.0	270	14	AAQ060682	Human brain expres
c 380	17	2.2	37925	22	AAK72372	Human immune/haema	c 453	16	2.0	271	21	AAK11751	Aspergillus niger
381	17	2.2	44602	22	AAK77611	Human immune/haema	c 454	16	2.0	281	16	AAQ99324	Mycobacterium kans
c 382	17	2.2	46954	23	ABL16830	Drosophila melanog	c 455	16	2.0	283	20	AAV89992	EST clone CW762.
383	17	2.2	51402	22	AAK72363	Human immune/haema	c 456	16	2.0	288	21	AAK42875	Human secreted exp
c 384	17	2.2	54863	22	AAK86026	Human immune/haema	c 457	16	2.0	288	22	AAK16141	Human breast cance
c 385	17	2.2	56743	22	AAK68202	Human immune/haema	c 458	16	2.0	289	22	AAK24984	Human breast cance
386	17	2.2	5743	22	AAK81760	Human immune/haema	c 459	16	2.0	289	22	AAI188396	Human polynucleoti
c 387	17	2.2	57728	22	AAK87588	Human immune/haema	c 460	16	2.0	295	22	AAK59438	Human KCC2 genomic
c 388	17	2.2	65921	21	AAK87588	Human 9p11 chromos	c 461	16	2.0	297	22	AAK88715	Human digestive sy
c 389	17	2.2	66685	22	AAK87588	Human genomic DNA	c 462	16	2.0	297	22	AAK531749	Human liver associ
c 390	17	2.2	73334	24	ABL34124	Human immune syste	c 463	16	2.0	300	20	AAK13982	Human gene express
c 391	17	2.2	73947	23	ABL07230	Drosophila melanog	c 464	16	2.0	300	20	AAK13758	Human gene express
c 392	17	2.2	73947	23	ABL07230	Human WRN genomic	c 465	16	2.0	305	22	AAH72363	Human cervical can
c 393	17	2.2	87350	18	AAK83003	Retinoblastoma bin	c 466	16	2.0	305	22	AAH72952	Human cervical can
c 394	17	2.2	162450	21	AAK86967	Arabidopsis thalia	c 467	16	2.0	311	18	AAH91705	Gene 056 fragmen
c 395	17	2.2	163319	21	AAK22306	Arabidopsis thalia	c 468	16	2.0	311	22	AAH70815	Human nervous syst
c 396	17	2.2	161590	21	AAK22306	Arabidopsis thalia	c 469	16	2.0	312	22	ABAI1572	Human polynucleoti
c 397	17	2.2	1230025	20	AAK31990	Nucleotide sequenc	c 470	16	2.0	312	22	AAK98002	Human colon cance
c 398	16	2.0	21	16	AAQ75615	Reverse transcript	c 471	16	2.0	322	21	AAK76345	Human immune/haema
c 399	16	2.0	21	16	AAK89839	E. coli DNA amplif	c 472	16	2.0	324	22	AAI90312	Human polynucleoti
c 400	16	2.0	25	20	AAK95990	HLA A-C gene PCR	c 473	16	2.0	326	22	AAH69480	Human cervical can
c 401	16	2.0	25	21	AAK96159	16S rRNA gene PCR	c 474	16	2.0	331	22	AAI90485	Human polynucleoti
c 402	16	2.0	25	21	AAK96564	HLA DRB345 gene PC	c 475	16	2.0	333	22	AAI90309	Human polynucleoti
c 403	16	2.0	25	21	AAK96862	HLA HLA-C gene PCR	c 476	16	2.0	339	22	AAI88707	Human polynucleoti
c 404	16	2.0	25	21	AAK96862	HLA HLA-C gene PCR	c 477	16	2.0	346	22	AAI80379	Human polynucleoti
c 405	16	2.0	25	21	AAK96862	Soybean 515002 reg	c 478	16	2.0	348	22	AAI85547	Human immune/haema
c 406	16	2.0	25	22	AAI62432	Target nucleic aci	c 479	16	2.0	350	22	AAK65095	Human immune/haema
c 407	16	2.0	35	15	AAQ70627	Primer to amplify	c 480	16	2.0	352	22	AAK76174	Human immune/haema
c 408	16	2.0	35	16	AAQ79590	Equus caballus Y c	c 481	16	2.0	352	22	AAK76175	Human immune/haema
c 409	16	2.0	41	20	AAK7590	Arabidopsis thalia	c 482	16	2.0	357	22	AAI90766	Human polynucleoti
c 410	16	2.0	51	21	AAK53103	Arabidopsis thalia	c 483	16	2.0	363	22	AAI88707	Human polynucleoti
c 411	16	2.0	53	21	AAK53102	Arabidopsis thalia	c 484	16	2.0	365	22	AAI88707	Human polynucleoti
c 412	16	2.0	54	15	AAK53104	Synthetic Cholera	c 485	16	2.0	369	20	AAZ24645	Human ovarian PCR-
c 413	16	2.0	57	18	AAK53104	Omega probe p302 u	c 486	16	2.0	371	22	AAK65884	Human lung cancer-
c 414	16	2.0	60	21	AAK53104	Arabidopsis thalia	c 487	16	2.0	371	22	AAI10305	Human Par-4 5' unt
c 415	16	2.0	76	18	AAK53104	Arabidopsis thalia	c 488	16	2.0	374	22	AAI88703	Human polynucleoti
c 416	16	2.0	106	22	AAK53100	Ribozyme (15') to s	c 489	16	2.0	376	21	AAI82403	Human polynucleoti
c 417	16	2.0	106	22	AAK53100	Human foetal liver	c 490	16	2.0	387	22	AAI85291	Human polynucleoti
c 418	16	2.0	106	22	AAK53100	Probe #18417 for g	c 491	16	2.0	387	22	AAI86502	Human polynucleoti
c 419	16	2.0	106	22	AAK53100	Human brain expres	c 492	16	2.0	387	22	AAI86502	Human polynucleoti
c 420	16	2.0	106	22	AAK53100	Human bone marrow	c 493	16	2.0	387	23	AAI86502	Human polynucleoti
c 421	16	2.0	106	22	AAK53100	Probe #16962 for g	c 494	16	2.0	389	22	AAI86502	DNA encoding novel
c 422	16	2.0	106	22	AAK53100	Probe #24548 used	c 495	16	2.0	389	22	AAI86502	Human polynucleoti
c 423	16	2.0	115	22	AAK53100	Human cervical can	c 496	16	2.0	391	22	AAI86502	Human immune/haema
c 424	16	2.0	121	22	AAK53100	MSH6 mutation corr	c 497	16	2.0	391	22	AAI86502	Human cDNA for an
c 425	16	2.0	121	22	AAK53100	Promoter region of	c 498	16	2.0	397	22	AAI86502	Human immune/haema
c 426	16	2.0	135	16	AAK53100	Human (2'-5') olij	c 499	16	2.0	398	22	AAI86502	Human polynucleoti
c 427	16	2.0	135	16	AAK53100	Bacteriophage Dp-1	c 500	16	2.0	401	22	AAK53100	Human neuregulin g
c 428	16	2.0	135	16	AAK53100	Human secreted pro	c 501	16	2.0	401	22	AAK53100	Human colon cancer
c 429	16	2.0	137	21	AAK53100	Mycobacterium kans	c 502	16	2.0	403	21	AAH31142	Human colon cancer
c 430	16	2.0	140	16	AAK53100	Human digestive nove	c 503	16	2.0	403	22	AAI83207	Human polynucleoti
c 431	16	2.0	152	22	AAK53100	Human digestive sy	c 504	16	2.0	403	22	AAI83207	Human polynucleoti
c 432	16	2.0	155	22	AAK53100	Human breast cance	c 505	16	2.0	405	22	AAI83207	Human contig polyn
c 433	16	2.0	158	22	AAK53100	EST clone HX110.	c 506	16	2.0	405	22	AAI83207	Human nervous syst
c 434	16	2.0	158	22	AAK53100	Genomic sequence #	c 507	16	2.0	408	22	AAI83207	Human secreted pro
c 435	16	2.0	158	22	AAK53100	Genomic sequence #	c 508	16	2.0	409	21	AAI83207	Human secreted pro
c 436	16	2.0	158	22	AAK53100	Human digestive sy	c 509	16	2.0	413	22	AAI83207	Human breast cance
c 437	16	2.0	158	22	AAK53100	Human digestive sy	c 510	16	2.0	413	22	AAI83207	Human breast cance
c 438	16	2.0	180	19	AAK53100	Human biallelic po	c 511	16	2.0	414	22	AAI83207	Human polynucleoti
c 439	16	2.0	180	19	AAK53100	Human secreted pro	c 512	16	2.0	414	22	AAI83207	Human polynucleoti
c 440	16	2.0	180	19	AAK53100	Human breast cance	c 513	16	2.0	415	21	AAI83207	Aspergillus niger
c 441	16	2.0	180	19	AAK53100	Human breast cance	c 514	16	2.0	415	21	AAI83207	Human polynucleoti
c 442	16	2.0	192	22	AAI16190	Soybean 515002 reg	c 515	16	2.0	420	20	AAI83207	Extended human sec
c 443	16	2.0	192	22	AAI16190	Drosophila melanog	c 516	16	2.0	420	20	AAI83207	Human polynucleoti
c 444	16	2.0	210	23	ABL24955	Human immune/haema	c 517	16	2.0	421	22	AAI83207	Human polynucleoti
c 445	16	2.0	219	22	AAK83145	Human KCC2 coding	c 518	16	2.0	422	22	AAI83207	Human breast cance
c 446	16	2.0	231	22	AAK83145	Human secreted pro	c 519	16	2.0	422	22	AAI83207	Human polynucleoti
c 447	16	2.0	244	21	AAK09447	Human secreted pro	c 520	16	2.0	422	23	AAI83207	DNA encoding novel
	16	2.0	249	21	AAK09447	Human secreted pro		16	2.0	424	21	AAI83207	Arabidopsis thalia
	16	2.0	255	22	AAI91733	Human polynucleoti		16	2.0				

c 521	16	2.0	424	22	AAH98722	Murine EST-derived	594	16	2.0	579	22	ABA64267	Human foetal liver
c 522	16	2.0	426	22	AAI84618	Human polynucleoti	595	16	2.0	579	22	AAK31407	Probe #9873 for ge
c 523	16	2.0	427	22	AAI90659	Human polynucleoti	596	16	2.0	579	22	AAK12737	Human brain expres
c 524	16	2.0	428	20	AAV87921	EST clone FF97. H	597	16	2.0	579	22	AAK38456	Human bone marrow
525	16	2.0	431	22	AAI81704	Human polynucleoti	598	16	2.0	579	22	AAI19256	Probe #9189 for ge
526	16	2.0	432	22	AAK72723	Human immune/haema	599	16	2.0	579	22	AAI14426	Probe #13112 used
c 527	16	2.0	437	22	AAI88950	Human polynucleoti	600	16	2.0	584	21	AAK40423	Arabidopsis thalia
c 528	16	2.0	438	22	AAI10590	Human breast cance	c 601	16	2.0	584	21	AAK40423	Human excretory re
529	16	2.0	439	22	AAK78629	Human immune/haema	c 602	16	2.0	584	22	AAI198605	Human kidney relat
530	16	2.0	440	22	AAI80553	Human polynucleoti	c 603	16	2.0	584	22	AAI163001	CDNA sequence #614
c 531	16	2.0	454	21	AAK82087	N. meningitidis pa	c 604	16	2.0	596	22	AAK09102	Human foetal liver
c 532	16	2.0	455	22	AAI92050	Human polynucleoti	605	16	2.0	596	22	AAK09102	Human brain expres
c 533	16	2.0	460	22	AAI12874	Human cDNA clone (606	16	2.0	596	22	AAK34992	Human bone marrow
534	16	2.0	469	22	AAI82196	Human polynucleoti	607	16	2.0	596	22	AAK140709	Probe #9395 used t
c 535	16	2.0	470	21	AAK40259	Arabidopsis thalia	608	16	2.0	599	24	ABK16292	Human lung tumour
c 536	16	2.0	472	22	ABA59453	Human foetal liver	609	16	2.0	600	23	AAK07502	Yeast YLR110C prom
c 537	16	2.0	472	22	ABA28109	Probe #6575 for ge	610	16	2.0	604	22	AAK77204	DNA encoding novel
c 538	16	2.0	472	22	AAK07691	Human brain expres	c 611	16	2.0	604	22	AAK19264	Human breast cance
c 539	16	2.0	472	22	AAK33505	Human bone marrow	c 612	16	2.0	610	22	AAI25033	Human breast cance
c 540	16	2.0	472	22	AAI16475	Probe #6408 for ge	613	16	2.0	615	22	AAH42839	Nucleotide sequenc
c 541	16	2.0	472	22	AAI39275	Probe #7961 used t	614	16	2.0	619	21	AAK47688	Arabidopsis thalia
c 542	16	2.0	472	22	AAI39275	Human contig polyn	615	16	2.0	620	21	AAK59908	Human secreted pro
543	16	2.0	473	22	AAK44844	Human ovarian tumo	616	16	2.0	624	22	AAH12855	Human cDNA clone (
544	16	2.0	476	22	AAH83118	Human secreted pro	617	16	2.0	627	17	AAI40734	DNA encoding Hmhk-
545	16	2.0	477	21	AAK06385	Human immune/haema	c 618	16	2.0	636	21	AAK59368	Human secreted pro
546	16	2.0	478	22	AAK79254	Peppermint plant O	c 619	16	2.0	640	22	AAK59368	CDNA encoding for
547	16	2.0	479	22	AAH87669	CDNA sequence from	620	16	2.0	640	22	AAK29121	CDNA encoding for
c 548	16	2.0	484	10	AAH92928	Barley Clone F. H	621	16	2.0	640	22	AAK64676	Human immune/haema
c 549	16	2.0	484	22	AAK89392	Mycobacterium kans	c 622	16	2.0	642	22	AAK95990	Mycobacterium tube
c 550	16	2.0	493	16	AAQ97352	Yeast promoter YLR	c 623	16	2.0	645	24	AAK62860	Human G protein-co
551	16	2.0	494	22	AAK07474	Human polynucleoti	624	16	2.0	651	22	AAH34407	Human colon cancer
552	16	2.0	496	22	AAI87743	Secreted protein E	625	16	2.0	653	19	AAV52938	Pig FPCD antigen e
553	16	2.0	506	20	AAK24081	Human ovarian can	626	16	2.0	653	22	AAK86438	Human immune/haema
c 554	16	2.0	507	22	AAK20623	Human immune/haema	627	16	2.0	654	22	AAK64037	Human immune/haema
c 555	16	2.0	508	22	AAK21224	Human signal pepti	c 628	16	2.0	662	22	AAK88730	Human digestive sy
556	16	2.0	518	21	AAK98140	Human immune/haema	c 629	16	2.0	662	22	AAK31764	Human liver associ
c 557	16	2.0	519	22	AAK81405	Human bone marrow	630	16	2.0	670	22	AAK86439	Human immune/haema
c 558	16	2.0	520	22	AAK36414	Human bone marrow	c 631	16	2.0	677	23	AAK68439	DNA encoding novel
559	16	2.0	524	16	AAI05515	Human neurogenic d	c 632	16	2.0	683	23	AAH84127	DNA encoding novel
560	16	2.0	524	18	AAK74889	Human neurogenic d	633	16	2.0	685	22	AAH99850	Human protein enco
c 561	16	2.0	528	19	AAV42930	Partial DNA sequen	634	16	2.0	689	21	AAK43438	Arabidopsis thalia
c 562	16	2.0	530	21	AAK53364	Drosophila melanog	635	16	2.0	694	8	AAK71218	Sequence of 5' fla
c 563	16	2.0	532	21	AAK40641	Arabidopsis thalia	636	16	2.0	694	8	AAK70210	Human nervous syst
564	16	2.0	532	21	AAK27129	Human inflammation	637	16	2.0	697	22	ABA14515	Human nervous syst
c 565	16	2.0	533	9	AAK80239	Region between loc	638	16	2.0	697	22	ABA16944	Human inflammatory
c 566	16	2.0	533	21	AAK78489	Plant SDF polynuc	639	16	2.0	700	22	AAH92015	Human inflammatory
c 567	16	2.0	539	22	AAI89209	Human polynucleoti	640	16	2.0	700	22	AAH92016	Human inflammatory
568	16	2.0	539	22	AAK57950	Human immune/haema	c 641	16	2.0	700	22	AAH92819	Human inflammatory
c 569	16	2.0	542	22	ABA62828	Human foetal liver	c 642	16	2.0	700	22	AAH92820	Human cDNA clone (
c 570	16	2.0	542	22	ABA30112	Probe #8578 for ge	c 643	16	2.0	705	22	AAH04500	Drosophila melanog
c 571	16	2.0	542	22	AAK11228	Human brain expres	c 644	16	2.0	705	23	ABL24197	Human neuroblastom
c 572	16	2.0	542	22	AAK37026	Human bone marrow	c 645	16	2.0	707	22	AAI95586	Arabidopsis thalia
c 573	16	2.0	542	22	AAI17873	Probe #7806 for ge	646	16	2.0	716	21	AAK39966	Human cervical can
c 574	16	2.0	542	22	AAI12846	Probe #11532 used	c 647	16	2.0	722	22	AAH70534	Human breast cance
c 575	16	2.0	543	22	AAK25687	H. pylori HPC172 e	c 648	16	2.0	732	22	AAK22026	Human immune/haema
576	16	2.0	544	22	AAH50674	Human tumour assoc	649	16	2.0	741	22	AAK82469	Human breast cance
577	16	2.0	546	22	ABA20255	Human nervous syst	650	16	2.0	744	21	AAK49543	Arabidopsis thalia
c 578	16	2.0	546	22	AAK32970	DNA encoding CARDI	651	16	2.0	748	21	AAK34335	Arabidopsis thalia
579	16	2.0	550	21	AAK94910	Cat flea hindgut a	652	16	2.0	748	21	AAK24936	DNA encoding a Sta
580	16	2.0	553	19	AAV34276	Human secreted pro	653	16	2.0	751	19	AAV53371	Human breast cance
581	16	2.0	553	23	AAK64348	DNA encoding novel	654	16	2.0	752	22	AAI21621	Human gene express
c 582	16	2.0	555	23	ABL21791	Drosophila melanog	c 655	16	2.0	754	22	AAI23289	Human neuroblastom
583	16	2.0	557	19	AAV34223	Human secreted pro	c 656	16	2.0	755	20	AAI217396	Human breast cance
c 584	16	2.0	561	22	AAK89051	Mannanase mannan b	c 657	16	2.0	755	22	AAI196715	Human neuroblastom
c 585	16	2.0	571	22	ABA62786	Human foetal liver	658	16	2.0	758	22	AAI23300	Human breast cance
c 586	16	2.0	571	22	ABA30079	Probe #8545 for ge	c 659	16	2.0	761	22	AAI96070	DNA encoding novel
c 587	16	2.0	571	22	AAI35685	Human musculoskele	c 660	16	2.0	772	23	AAI95469	Human neuroblastom
c 588	16	2.0	571	22	AAK11184	Human brain expres	c 661	16	2.0	775	22	AAI95900	Human neuroblastom
c 589	16	2.0	571	22	AAK36991	Human bone marrow	662	16	2.0	775	22	AAK29120	CDNA encoding for
c 590	16	2.0	571	22	AAI17833	Probe #7766 for ge	663	16	2.0	775	22	AAK63943	Human immune/haema
c 591	16	2.0	571	22	AAI42803	Probe #11489 used	664	16	2.0	776	20	AAK52955	Human prostate tum
c 592	16	2.0	572	22	AAI41139	Probe #9825 used t	c 665	16	2.0	777	20	AAK504945	DNA encoding novel
593	16	2.0	574	22	AAI19901	Human breast cance	666	16	2.0	803	20	AAK04317	Human secreted pro

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667	16	2.0	803	22	AA161003	Human polynucleoti	740	16	2.0	1255	7	AA160519	CDNA of clone lamb
668	16	2.0	811	22	AA106357	Human reproductive	741	16	2.0	1257	22	AA133238	Human colon cancer
669	16	2.0	815	22	AA123913	Human breast cance	742	16	2.0	1274	22	AA150331	CDNA encoding nove
670	16	2.0	828	22	AA196002	Human neuroblastom	743	16	2.0	1281	22	AA152118	CDNA encoding nove
671	16	2.0	833	22	AA197396	Human neuroblastom	744	16	2.0	1281	22	AA152118	Drosophila melanog
672	16	2.0	840	22	AA198302	Human MSH6 fragmen	745	16	2.0	1284	23	AA106047	Colon cancer assoc
673	16	2.0	853	22	AA171074	Human MSH6 fragmen	746	16	2.0	1298	20	AA100056	MHC class II anti
674	16	2.0	853	22	AA171074	DNA encoding novel	747	16	2.0	1302	12	AA111112	Arabidopsis thalia
675	16	2.0	860	22	AA179359	Plant viral moveme	748	16	2.0	1317	21	AA1046130	Arabidopsis thalia
676	16	2.0	860	22	AA193247	Human polynucleoti	749	16	2.0	1323	21	AA190584	Maize ORF2540
677	16	2.0	865	22	AA144865	Human polynucleoti	750	16	2.0	1338	21	AA190584	Human ORF2540
678	16	2.0	867	22	AA194090	Arabidopsis thalia	751	16	2.0	1342	6	AA150443	EPO clone lambda-h
679	16	2.0	868	22	AA132677	Human neuroblastom	752	16	2.0	1342	7	AA160513	CDNA of clone lamb
680	16	2.0	877	20	AA136696	Human neuroblastom	753	16	2.0	1348	19	AA134289	Human secreted pro
681	16	2.0	880	21	AA136696	Human neuroblastom	754	16	2.0	1348	21	AA134289	Arabidopsis thalia
682	16	2.0	890	21	AA136696	Human neuroblastom	755	16	2.0	1348	21	AA134289	CDNA encoding nove
683	16	2.0	904	18	AA197690	Human neuroblastom	756	16	2.0	1364	22	AA108651	Human CDNA encodin
684	16	2.0	904	18	AA197690	Human neuroblastom	757	16	2.0	1364	22	AA108651	Human atrial natri
685	16	2.0	910	22	AA146494	Human neuroblastom	758	16	2.0	1372	22	AA108651	Human secreted pro
686	16	2.0	912	22	AA146494	Human neuroblastom	759	16	2.0	1378	22	AA108651	Nucleotide sequenc
687	16	2.0	926	20	AA125151	Arabidopsis thalia	760	16	2.0	1389	21	AA108651	Human secreted pro
688	16	2.0	936	22	AA108651	Human neuroblastom	761	16	2.0	1396	23	AA108651	Drosophila melanog
689	16	2.0	940	22	AA108651	Human neuroblastom	762	16	2.0	1408	22	AA108651	APEX-3 CDNA. Homo
690	16	2.0	947	22	AA108651	Human neuroblastom	763	16	2.0	1410	21	AA108651	Arabidopsis thalia
691	16	2.0	964	22	AA108651	Human neuroblastom	764	16	2.0	1437	22	AA108651	Human endocrine po
692	16	2.0	976	18	AA108651	Human neuroblastom	765	16	2.0	1452	23	AA108651	DNA encoding novel
693	16	2.0	990	21	AA108651	Human neuroblastom	766	16	2.0	1462	22	AA108651	Human polynucleoti
694	16	2.0	1001	21	AA108651	Human neuroblastom	767	16	2.0	1462	22	AA108651	Human polynucleoti
695	16	2.0	1001	21	AA108651	Human neuroblastom	768	16	2.0	1494	22	AA108651	Human prostate can
696	16	2.0	1001	21	AA108651	Human neuroblastom	769	16	2.0	1494	22	AA108651	Human immunoglobul
697	16	2.0	1001	21	AA108651	Human neuroblastom	770	16	2.0	1500	21	AA108651	Human full-length
698	16	2.0	1001	21	AA108651	Human neuroblastom	771	16	2.0	1500	21	AA108651	Drosophila melanog
699	16	2.0	1001	21	AA108651	Human neuroblastom	772	16	2.0	1526	21	AA108651	Arabidopsis thalia
700	16	2.0	1001	21	AA108651	Human neuroblastom	773	16	2.0	1536	18	AA108651	Rat peromone rece
701	16	2.0	1001	21	AA108651	Human neuroblastom	774	16	2.0	1536	18	AA108651	Arabidopsis thalia
702	16	2.0	1001	21	AA108651	Human neuroblastom	775	16	2.0	1536	18	AA108651	Arabidopsis thalia
703	16	2.0	1001	21	AA108651	Human neuroblastom	776	16	2.0	1536	18	AA108651	Arabidopsis thalia
704	16	2.0	1001	21	AA108651	Human neuroblastom	777	16	2.0	1536	18	AA108651	Arabidopsis thalia
705	16	2.0	1001	21	AA108651	Human neuroblastom	778	16	2.0	1536	18	AA108651	Arabidopsis thalia
706	16	2.0	1001	21	AA108651	Human neuroblastom	779	16	2.0	1536	18	AA108651	Arabidopsis thalia
707	16	2.0	1001	21	AA108651	Human neuroblastom	780	16	2.0	1536	18	AA108651	Arabidopsis thalia
708	16	2.0	1001	21	AA108651	Human neuroblastom	781	16	2.0	1536	18	AA108651	Arabidopsis thalia
709	16	2.0	1001	21	AA108651	Human neuroblastom	782	16	2.0	1536	18	AA108651	Arabidopsis thalia
710	16	2.0	1001	21	AA108651	Human neuroblastom	783	16	2.0	1536	18	AA108651	Arabidopsis thalia
711	16	2.0	1001	21	AA108651	Human neuroblastom	784	16	2.0	1536	18	AA108651	Arabidopsis thalia
712	16	2.0	1001	21	AA108651	Human neuroblastom	785	16	2.0	1536	18	AA108651	Arabidopsis thalia
713	16	2.0	1001	21	AA108651	Human neuroblastom	786	16	2.0	1536	18	AA108651	Arabidopsis thalia
714	16	2.0	1001	21	AA108651	Human neuroblastom	787	16	2.0	1536	18	AA108651	Arabidopsis thalia
715	16	2.0	1001	21	AA108651	Human neuroblastom	788	16	2.0	1536	18	AA108651	Arabidopsis thalia
716	16	2.0	1001	21	AA108651	Human neuroblastom	789	16	2.0	1536	18	AA108651	Arabidopsis thalia
717	16	2.0	1001	21	AA108651	Human neuroblastom	790	16	2.0	1536	18	AA108651	Arabidopsis thalia
718	16	2.0	1001	21	AA108651	Human neuroblastom	791	16	2.0	1536	18	AA108651	Arabidopsis thalia
719	16	2.0	1001	21	AA108651	Human neuroblastom	792	16	2.0	1536	18	AA108651	Arabidopsis thalia
720	16	2.0	1001	21	AA108651	Human neuroblastom	793	16	2.0	1536	18	AA108651	Arabidopsis thalia
721	16	2.0	1001	21	AA108651	Human neuroblastom	794	16	2.0	1536	18	AA108651	Arabidopsis thalia
722	16	2.0	1001	21	AA108651	Human neuroblastom	795	16	2.0	1536	18	AA108651	Arabidopsis thalia
723	16	2.0	1001	21	AA108651	Human neuroblastom	796	16	2.0	1536	18	AA108651	Arabidopsis thalia
724	16	2.0	1001	21	AA108651	Human neuroblastom	797	16	2.0	1536	18	AA108651	Arabidopsis thalia
725	16	2.0	1001	21	AA108651	Human neuroblastom	798	16	2.0	1536	18	AA108651	Arabidopsis thalia
726	16	2.0	1001	21	AA108651	Human neuroblastom	799	16	2.0	1536	18	AA108651	Arabidopsis thalia
727	16	2.0	1001	21	AA108651	Human neuroblastom	800	16	2.0	1536	18	AA108651	Arabidopsis thalia
728	16	2.0	1001	21	AA108651	Human neuroblastom	801	16	2.0	1536	18	AA108651	Arabidopsis thalia
729	16	2.0	1001	21	AA108651	Human neuroblastom	802	16	2.0	1536	18	AA108651	Arabidopsis thalia
730	16	2.0	1001	21	AA108651	Human neuroblastom	803	16	2.0	1536	18	AA108651	Arabidopsis thalia
731	16	2.0	1001	21	AA108651	Human neuroblastom	804	16	2.0	1536	18	AA108651	Arabidopsis thalia
732	16	2.0	1001	21	AA108651	Human neuroblastom	805	16	2.0	1536	18	AA108651	Arabidopsis thalia
733	16	2.0	1001	21	AA108651	Human neuroblastom	806	16	2.0	1536	18	AA108651	Arabidopsis thalia
734	16	2.0	1001	21	AA108651	Human neuroblastom	807	16	2.0	1536	18	AA108651	Arabidopsis thalia
735	16	2.0	1001	21	AA108651	Human neuroblastom	808	16	2.0	1536	18	AA108651	Arabidopsis thalia
736	16	2.0	1001	21	AA108651	Human neuroblastom	809	16	2.0	1536	18	AA108651	Arabidopsis thalia
737	16	2.0	1001	21	AA108651	Human neuroblastom	810	16	2.0	1536	18	AA108651	Arabidopsis thalia
738	16	2.0	1001	21	AA108651	Human neuroblastom	811	16	2.0	1536	18	AA108651	Arabidopsis thalia
739	16	2.0	1001	21	AA108651	Human neuroblastom	812	16	2.0	1536	18	AA108651	Arabidopsis thalia

c 813	16	2.0	1790	21	AAC34196	Arabidopsis thalia	886	16	2.0	2533	22	AAC88111	Human PLEXHT-42 nu
814	16	2.0	1794	23	AAS70163	DNA encoding novel	887	16	2.0	2544	22	AAC17822	Human cDNA sequenc
815	16	2.0	1824	21	AAT77128	Human ORFX ORF2683	c 888	16	2.0	2558	22	AAF55249	Nucleotide sequenc
816	16	2.0	1842	23	AAS72632	DNA encoding novel	c 889	16	2.0	2588	22	AAH73967	Human reducing aye
817	16	2.0	1844	19	AAV24018	Human BHF1 coding	890	16	2.0	2625	21	AAH16658	Human secreted pro
818	16	2.0	1845	15	AZ298400	Canine betat-adren	891	16	2.0	2627	21	AAH70077	Human ovarian carc
819	16	2.0	1875	15	AAQ58758	Rat glucagon recep	892	16	2.0	2627	21	AAH55681	Human ovarian tumo
820	16	2.0	1907	22	AAH19183	Human secreted pro	c 893	16	2.0	2630	23	AA569483	DNA encoding novel
821	16	2.0	1922	15	AAQ66639	Mouse Activin rece	c 894	16	2.0	2633	23	AA569279	DNA encoding novel
c 822	16	2.0	1922	20	AAZ09846	Human MALK-1 clone	c 895	16	2.0	2635	20	AAV84521	Human secreted pro
823	16	2.0	1926	22	AAH19220	Human secreted pro	896	16	2.0	2658	23	ABH3304	Drosophila melanog
824	16	2.0	1944	21	AAH69015	Bacteriophage 44AH	c 897	16	2.0	2665	22	AA501479	Human secreted pro
825	16	2.0	1954	22	AAQ66894	Human EXMAD-5 codi	898	16	2.0	2674	21	AAH93443	GFP-HSC70 fusion g
c 826	16	2.0	1979	22	AAH18361	Human cDNA sequenc	899	16	2.0	2682	21	AAH88863	Human dentin matril
c 827	16	2.0	1980	20	AAH58808	Human leukaemia-as	c 900	16	2.0	2704	23	ABH13675	Drosophila melanog
828	16	2.0	1986	21	AAQ95489	Human secreted pro	c 901	16	2.0	2705	23	ABH13675	Drosophila melanog
c 829	16	2.0	2027	23	AAS90594	DNA encoding novel	c 902	16	2.0	2719	22	AAH13886	Human cDNA sequenc
c 830	16	2.0	2054	21	AAQ59693	Human secreted pro	c 903	16	2.0	2720	23	ABH13886	Human cDNA sequenc
c 831	16	2.0	2058	14	AAQ41227	Clone GP46 encodin	904	16	2.0	2720	23	ABH13886	Human EXCS encodin
c 832	16	2.0	2068	22	AAK81547	Human immune/haema	905	16	2.0	2730	22	AAH84293	Human EXCS encodin
833	16	2.0	2081	21	AAH76582	Human ORFX ORF2137	906	16	2.0	2732	20	AAH05810	Mouse pheromone re
834	16	2.0	2089	22	AAH57139	DNA encoding Dros	c 907	16	2.0	2756	22	AAH17562	Human cDNA sequenc
835	16	2.0	2089	23	ABH13921	Drosophila melanog	c 908	16	2.0	2771	22	AAH17350	Human cDNA sequenc
836	16	2.0	2089	24	ABH19790	Mouse ischaemic co	909	16	2.0	2840	21	AAH78596	Human PRO4993 nucl
c 837	16	2.0	2094	21	AAH99018	Human pancreatic c	c 910	16	2.0	2865	23	ABH22130	Drosophila melanog
c 838	16	2.0	2101	17	AAH11743	Rat kynurenine ami	c 911	16	2.0	2895	22	AAF55248	Nucleotide sequenc
c 839	16	2.0	2114	20	AAH19958	Rat tango-76 encod	c 912	16	2.0	2918	22	AAF55252	Human secreted pro
c 840	16	2.0	2118	21	AAH51464	Arabidopsis thalia	913	16	2.0	2923	20	AAH04326	Human stomach canc
841	16	2.0	2127	22	AAH85819	HOAT1 DNA. Homo s	c 914	16	2.0	2925	22	AAH193896	Human cDNA sequenc
842	16	2.0	2174	21	AAH53823	Sequence encoding	c 915	16	2.0	2925	22	AAH16302	Human cDNA sequenc
c 843	16	2.0	2198	20	AAH22779	Rat SOCS17 cDNA.	c 916	16	2.0	2957	22	AAH86215	Human immune/haema
c 844	16	2.0	2198	20	AAH22773	Rat SOCS17 cDNA.	c 917	16	2.0	3000	21	AAH65523	Porcine BAC-PIGF2-
845	16	2.0	2198	24	ABA03615	Human 34P3D7 cDNA.	c 918	16	2.0	3014	22	AAF55247	Nucleotide sequenc
846	16	2.0	2198	24	ABA03616	Human 34P3D7 mRNA.	c 919	16	2.0	3029	23	ABH23754	Drosophila melanog
847	16	2.0	2201	21	AAZ43777	Human fetal brain	c 920	16	2.0	3043	22	AAF55253	Drosophila melanog
848	16	2.0	2210	23	ABH24954	Drosophila melanog	921	16	2.0	3045	23	ABH19459	Drosophila melanog
849	16	2.0	2233	22	AAH26418	Pseudomonas sp hea	c 922	16	2.0	3089	23	ABH04273	Nucleotide sequenc
c 850	16	2.0	2239	23	ABH11831	Drosophila melanog	c 923	16	2.0	3092	22	AAF55257	Arabidopsis thalia
c 851	16	2.0	2243	22	AAH73362	Human cervical can	c 924	16	2.0	3129	21	AAH43286	Nucleotide sequenc
c 852	16	2.0	2253	21	AAH99127	Human pancreatic c	c 925	16	2.0	3136	22	AAF55250	Drosophila melanog
c 853	16	2.0	2275	22	AAH31140	Human diagnostic a	926	16	2.0	3136	23	ABH19748	Drosophila melanog
c 854	16	2.0	2285	17	AAH13426	Humicola insolens	c 927	16	2.0	3152	23	ABH13448	Drosophila melanog
c 855	16	2.0	2285	19	AAH19376	Humicola insolens	c 928	16	2.0	3159	23	ABH22238	Nucleotide sequenc
856	16	2.0	2290	22	AAH29606	Human endocrine po	c 929	16	2.0	3170	22	AAF55251	Drosophila melanog
857	16	2.0	2297	23	AAH82982	DNA encoding novel	c 930	16	2.0	3223	23	ABH08588	Human c-myc oncoge
858	16	2.0	2303	18	AAH47338	Murine development	c 931	16	2.0	3225	19	AAV20467	Human immune syste
859	16	2.0	2303	20	AAH18506	Murine del-1 encod	c 932	16	2.0	3231	24	ABH34288	Nucleotide sequenc
860	16	2.0	2308	18	AAH47339	Murine del-1 trunc	c 933	16	2.0	3253	22	AAF55254	Nucleotide sequenc
861	16	2.0	2308	20	AAH18507	Truncated murine d	c 934	16	2.0	3253	22	AAF55256	Nucleotide sequenc
c 862	16	2.0	2309	23	ABH24854	Drosophila melanog	c 935	16	2.0	3254	22	AAF55255	Nucleotide sequenc
c 863	16	2.0	2314	22	AAH76171	Human immune/haema	c 936	16	2.0	3255	22	AAF55244	Nucleotide sequenc
c 864	16	2.0	2318	22	AAH40855	DNA encoding nove	c 937	16	2.0	3255	22	AAF55258	Nucleotide sequenc
865	16	2.0	2343	20	AAH24811	Human secreted pro	c 938	16	2.0	3255	22	AAF55259	Nucleotide sequenc
c 866	16	2.0	2348	22	AAH46914	cDNA encoding huma	c 939	16	2.0	3255	22	AAF55260	Nucleotide sequenc
867	16	2.0	2350	22	AAH198954	Human excretory re	c 940	16	2.0	3282	21	AAH50241	Arabidopsis thalia
868	16	2.0	2350	22	AAH163304	Human kidney relat	c 941	16	2.0	3282	22	AAH167268	GABApie cDNA seque
869	16	2.0	2370	19	AAH68069	Maize-optimized DN	c 942	16	2.0	3306	13	AAQ22202	A. chrysogenum pho
870	16	2.0	2403	17	AAH13955	Maize-optimized VI	c 943	16	2.0	3306	13	AAQ23005	Phosphoglycerate k
871	16	2.0	2403	17	AAH14004	Maize-optimized-B.	c 944	16	2.0	3306	14	AAQ48534	PGK. Acremonium c
872	16	2.0	2403	19	AAH68065	Maize-optimized DN	c 945	16	2.0	3309	21	AAH21886	Human breast and o
873	16	2.0	2403	19	AAH16177	Maize-optimized DN	c 946	16	2.0	3345	23	ABH12550	Drosophila melanog
874	16	2.0	2424	23	AAH75668	Human encoding nove	c 947	16	2.0	3362	22	ABH18396	Human nervous syst
c 875	16	2.0	2434	22	AAH36971	Human musculuskele	c 948	16	2.0	3391	22	AAH88698	Mannanase coding s
c 876	16	2.0	2438	19	AAH36867	Mus musculus SOCS1	c 949	16	2.0	3422	22	AAH03358	Human reproductive
877	16	2.0	2444	9	AAH81254	cDNA sequence in p	c 950	16	2.0	3422	22	AAH03360	Human immunoglobul
878	16	2.0	2444	17	AAH13964	VIP3A(a) synthetic	951	16	2.0	3422	22	AAH28909	Human immunoglobul
879	16	2.0	2444	18	AAH74011	B. cereus VIP3A(a)	c 952	16	2.0	3422	22	AAH28911	Human phosphodiester
880	16	2.0	2444	19	AAH16190	DNA for maize opti	c 953	16	2.0	3427	21	AAH09591	Human cDNA sequenc
881	16	2.0	2502	21	AAH62679	Human NeuroBl gene	954	16	2.0	3434	22	AAH14440	Drosophila melanog
882	16	2.0	2505	21	AAH99819	Human secreted pro	955	16	2.0	3486	23	ABH126562	Drosophila melanog
883	16	2.0	2506	22	AAH07439	Human reproductive	c 956	16	2.0	3540	23	ABH02062	Drosophila melanog
884	16	2.0	2506	22	AAH162735	Human breast or ov	c 957	16	2.0	3551	23	ABH17756	Drosophila melanog
885	16	2.0	2527	23	ABH21520	Drosophila melanog	958	16	2.0	3559	22	AAH160356	Human polynucleoti

ALIGNMENTS

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ALIGNMENTS

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ALIGNMENTS

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Db 361 CAGACCGGACAGGAGGCGGATGAGCGACACACACAAACACAGACACACACGCC 420
QY 421 AGTCCCGAGGCGCCAGTAATGGAGAGCGCCCAAAAAGAGAACCCAGCAGCTGAAAGTCGGG 480
Db 421 AGTCCCGAGGCGCCAGTAATGGAGAGCGCCCAAAAAGAGAACCCAGCAGCTGAAAGTCGGG 480
QY 481 ATCTACACTGGGACGACAGAGAGATCAGGATACAGCTGAGATCCCACTGCCG 540
Db 481 ATCTACACTGGGACGACAGAGAGATCAGGATACAGCTGAGATCCCACTGCCG 540
QY 541 ACATGGAAGTGATCTGCAAGAGCTGCATCAGTCAAAACACCGGGGATAAATCTGGATTG 600
Db 541 ACATGGAAGTGATCTGCAAGAGCTGCATCAGTCAAAACACCGGGGATAAATCTGGATTG 600
QY 601 GGTTCGGGCTCAAGTGAAGATAATACCTAAAGAGGACACTGTAATAATGCCAAGCA 560
Db 601 GGTTCGGGCTCAAGTGAAGATAATACCTAAAGAGGACACTGTAATAATGCCAAGCA 560
QY 661 GGTGAAGAGCAACCAAGTTTAAATGAAGACAAGCTGAAACAACCAAGCTGCTTTTAT 720
Db 661 GGTGAAGAGCAACCAAGTTTAAATGAAGACAAGCTGAAACAACCAAGCTGCTTTTAT 720
QY 721 ATTAGATATTGACTTAACATCTCAATAAGTTTTCAGCTTTTACCAAAAAA 780
Db 721 ATTAGATATTGACTTAACATCTCAATAAGTTTTCAGCTTTTACCAAAAAA 780
QY 781 A 781
Db 781 A 781

RESULT 2
AA537109
ID AA537109 standard; cDNA; 396 BP.
XX AA537109;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human diagnostic and therapeutic gene #167.
XX
KW Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss.
XX
OS Homo sapiens.
XX
PN WO200166753-A2.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-US07787.
XX
PR 09-MAR-2000; 2000US-0188609.
XX
PA (CHIR) CHIRON CORP.
XX (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis WA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Randazzo F, Kennedy GC, Pot D, Kassam A, Lamson G;
PI Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX
DR WPI; 2001-530177/58.
XX
XX New polynucleotides and polypeptides, useful for diagnosis and
PT treatment of breast, lung and colon cancer -
XX
XX Claim 1; Page 638; 1193pp; English.
XX
XX The invention relates to new polynucleotides and polypeptides, useful for
CC diagnosis and treatment of breast, lung and colon cancer. The sequences
CC can be used in detecting differentially expressed genes correlated with a
CC cancerous state of a mammalian cell, comprising detecting at least one

CC differentially expressed gene product in a test sample derived from a
CC cell suspected of being cancerous. They can also be used to inhibit
CC tumour growth by modulating expression of a gene product. AA536943-
CC AA539338 represent novel human diagnostic and therapeutic coding
CC sequences of the invention.
XX
SQ Sequence 396 BP; 82 A; 97 C; 146 G; 71 T; 0 other;

Query Match 50.1%; Score 391; DB 22; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.2e-172; Indels 0; Gaps 0;
Matches 391; Conservative 0; Mismatches 0;

QY 2 CGCGCGAGCTGTGAGCCGCGGACTCGGGTCCCTGAGGTCTGGATTCTTTCTCCGCTACTG 61
Db 1 CGCGCGAGCTGTGAGCCGCGGACTCGGGTCCCTGAGGTCTGGATTCTTTCTCCGCTACTG 60
QY 62 AGACACGGGGGTAGTTCACAGGAGATCCAACTGGGAGTTGAAGTGTGAGTGAGAGTG 121
Db 61 AGACACGGGGGTAGTTCACAGGAGATCCAACTGGGAGTTGAAGTGTGAGTGAGAGTG 120
QY 122 AAGAGGAACCAAGCAGGCTTCCCGAGGGTTGTGTGTCAGTGACTCAGAGTGAGAGGCC 181
Db 121 AAGAGGAACCAAGCAGGCTTCCCGAGGGTTGTGTGTCAGTGACTCAGAGTGAGAGGCC 180
QY 182 TCGAAGTCTGCTGCTCTCATGCGGTGCCAGCCCATGGACCTTCTGTCGTCACGG 241
Db 181 TCGAAGTCTGCTGCTCTCATGCGGTGCCAGCCCATGGACCTTCTGTCGTCACGG 240
QY 242 CCATAACTAGGAGGAAGGAGGCGGAGAGTGGAGGGCTCAGGCGAAGCTGGGGTGCT 301
Db 241 CCATAACTAGGAGGAAGGAGGCGGAGAGTGGAGGGCTCAGGCGAAGCTGGGGTGCT 300
QY 302 GTTGGGGTATCCGATCCCAGAACACCTGGAACCCCGACAGAGATTCTTGACTCCCC 361
Db 301 GTTGGGGTATCCGATCCCAGAACACCTGGAACCCCGACAGAGATTCTTGACTCCCC 360
QY 362 AGACGGGACCAAGAGAGGAGGCGGATGACG 392
Db 361 AGACGGGA/CAGAGAGGAGGCGGATGACG 391

RESULT 3
AAH64751
ID AAH64751 standard; cDNA; 762 BP.
XX
AC AAH64751;
XX
DT 11-SEP-2001 (first entry)
XX
DE Human secreted protein cDNA, SEQ ID NO: 27.
XX
KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
KW GENSET; ss.
XX
OS Homo sapiens.
XX
PN WO200142451-A2.
XX
PD 14-JUN-2001.
XX
PF 07-DEC-2000; 2000WO-IB01938.
XX
PR 08-DEC-1999; 99US-0169629.
PR 06-MAR-2000; 2000US-0187470.
XX
XX (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Bougueleret L, Jobert S;
XX
DR WPI; 2001-367870/38.
DR P-PSDB; AAG89148.
XX
PT Full length GENSET human nucleic acids encoding potentially secreted

PT	proteins, useful in gene therapy and vaccination against a variety of	
PT	diseases, and for diagnosis of those diseases -	
XX		
PS	Claim 7; Page 586; 921pp; English.	
XX		
CC	The invention relates to full length GENSET human nucleic acids encoding	
CC	potentially secreted proteins. The nucleic acids and the polypeptides	
CC	they encode may be used in the prevention, treatment and diagnosis of	
CC	diseases associated with inappropriate GENSET gene expression. For	
CC	example, they be used to treat disorders associated with decreased	
CC	GENSET gene expression by rectifying mutations or deletions in a	
CC	patient's genome that affect the activity of GENSET or by supplementing	
CC	the patients own production of GENSET polypeptides. Conversely,	
CC	antisense nucleic acid molecules may be administered to down regulate	
CC	GENSET expression by binding with the cells' own genes and preventing	
CC	their expression. The sense and antisense nucleic acids may also be	
CC	used as DNA probes in diagnostic assays to detect and quantitate the	
CC	presence of similar nucleic acid sequences in samples, and hence to	
CC	determine which patients may be in need of restorative therapy.	
CC	The GENSET polypeptides may be used as antigens in the production of	
CC	antibodies and in assays to identify modulators (agonists and	
CC	antagonists) of GENSET polypeptide expression and activity. The	
CC	present sequence is a GENSET nucleic acid of the invention.	
XX		
SQ	Sequence 762 BP; 220 A; 192 C; 186 G; 164 T; 0 other;	
	Query Match 49.9%; Score 390; DB 22; Length 762;	
	Best Local Similarity 100.0%; Pred. No. 3.4e-172;	
	Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	392 GACACACACAAACACAGAACCCACAGCCAGTCCAGGAGCCAGTAATGGAGGCCCA 451	
DB	370 GACACACACAAACACAGAACCCACAGCCAGTCCAGGAGCCAGTAATGGAGGCCCA 429	
QY	452 AAAAGAAGAACCCAGCAGCTGAAAGTCGGGATCCTACACCTGGCGCAGCAGACAAAGA 511	
DB	430 AAAAGAAGAACCCAGCAGCTGAAAGTCGGGATCCTACACCTGGCGCAGCAGACAAAGA 489	
QY	512 TCAGGTATACAGTCCAGTCCAGTCCGACATGGAAGGTGATCTGCAAGAGTGCATCA 571	
DB	490 TCAGGTATACAGTCCAGTCCAGTCCGACATGGAAGGTGATCTGCAAGAGTGCATCA 549	
QY	572 GTCAAACACCGGGATAAATCTGGATTGGTTCCGGCGTCAAGGTGAAGATAATACCTA 631	
DB	550 GTCAAACACCGGGATAAATCTGGATTGGTTCCGGCGTCAAGGTGAAGATAATACCTA 609	
QY	632 AAGAGGAACACTGTAAATGTCAGAACGAGTGAAGAGCACCAACACAGTTTAATGAAGA 691	
DB	610 AAGAGGAACACTGTAAATGTCAGAACGAGTGAAGAGCACCAACACAGTTTAATGAAGA 669	
QY	692 CAAGCTGAACACACGCAAGCTGGTTTATATTAGATATTTGACTTAAACTATCTCAATAA 751	
DB	670 CAAGCTGAACACACGCAAGCTGGTTTATATTAGATATTTGACTTAAACTATCTCAATAA 729	
QY	752 AGTTTTCAGCTTTTACCACAAAAA 781	
DB	730 AGTTTTCAGCTTTTACCACAAAAA 759	
RESULT 4		
AAF68151		
ID	AAF68151 standard; cDNA; 399 BP.	
XX		
AC	AAF68151;	
XX		
DT	12-APR-2001 (first entry)	
XX		
DE	Human lung tumour protein related nucleotide sequence SEQ ID NO:69.	
XX		
KW	Human; lung cancer; lung tumour; lung tumour protein; gene therapy;	
KW	lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;	
KW	cytostatic; antisense inhibition; ss.	
XX		

Db 190 GTCAACACCGGGATAAATCTGGATTTCGGGTCCTCAAGGTGAAGATAATACCTA 249
QY 632 AAGAGGAACACTCTAAATGCCAGAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGA 691
Db 250 AAGAGGAACACTCTAAATGCCAGAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGA 309
QY 692 CAAGCTGAAACACGCAAGCTGTTTATATTAGATATTGTGACTTAAACTATCTCAATAA 751
Db 310 CAAGCTGAAACACGCAAGCTGTTTATATTAGATATTGTGACTTAAACTATCTCAATAA 369
QY 752 AGTTTTCAGCTTTCACCAA 771
Db 370 AGTTTTCAGCTTTCACCAA 389
RESULT 5
AAF68851
ID AAF68851 standard; cDNA; 457 BP.
AC AAF68851:
XX
DT 12-APR-2001 (first entry)
XX
DE Human lung tumour protein related nucleotide sequence SEQ ID NO:790.
XX
KW Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
KW lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
KW cytostatic; antisense inhibition; ss.
XX
OS Homo sapiens.
XX
PN WO200100828-A2.
XX
PD 04-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-0518061.
XX
PR 30-JUN-1999; 99US-0346492.
PR 15-OCT-1999; 99US-0419356.
PR 17-DEC-1999; 99US-0466867.
PR 30-DEC-1999; 99US-0476300.
PR 06-MAR-2000; 2000US-0519642.
PR 22-MAR-2000; 2000US-0533077.
PR 10-APR-2000; 2000US-0546259.
PR 27-APR-2000; 2000US-0560406.
PR 05-JUN-2000; 2000US-0589184.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
PI Retter MW, Mannion J;
XX
XX WPI; 2001-071488/08.
XX
XX Lung tumor-associated proteins and the nucleic acids that encode them,
PT useful for preventing, diagnosing and treating lung cancer -
XX
XX Claim 4; Page 412; 436pp; English.
XX
XX The present invention describes immunogenic portions of lung tumour-
CC associated proteins (I) and the nucleic acids (NAS) that encode them.
CC (I) have cytostatic activity and can be used in gene therapy, antisense
CC inhibition and in vaccines. The NAS and the lung tumour-associated
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with their inappropriate expression,
CC especially lung cancers. For example, the NAS may be administered to
CC treat diseases by rectifying mutations or deletions in a patient's genome
CC that affect the activity of the protein by expressing inactive proteins
CC or to supplement the patients own production of (I). Additionally, the
CC NAS may be used to produce the lung-tumour associated protein, according
CC to standard recombinant DNA methodology. Conversely, antisense NA
CC molecules may be administered to down regulate protein expression by

CC binding with the cells own genes and preventing their expression. The NA
CC and complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar NA sequences in
CC samples, and hence which patients may be in need of treatment for lung
CC cancer. The (I) may be used as antigens in the production of antibodies
CC and in assays to identify modulators (agonists and antagonists) of the
CC expression and activity of the protein. AAF68083 to AAF68878 and
CC AAB576848 to AAB76878 represent human lung tumour protein related
CC nucleotide and protein sequences which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 457 BP; 146 A; 105 C; 121 G; 85 T; 0 other;
Query Match 47.1%; Score 368; DB 22; Length 457;
Best Local Similarity 100.0%; Pred. No. 6.5e-162;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 392 GACACACAAACACAGCAACACAGCCAGTCCCGAGAGCCCGAGTATGGAGAGCCCCA 451
Db 90 GACACACAAACACAG/ACCACACAGCCAGTCCCGAGAGCCCGAGTATGGAGAGCCCCA 149
QY 452 AAAAGAAGAACACAGCTGAAAGTCGGGATCTTACACCTGGCGAGCAGACAGAGAAGA 511
Db 150 AAAAGAAGAACACAGCTGAAAGTCGGGATCTTACACCTGGCGAGCAGACAGAGAAGA 209
QY 512 TCAGGATACAGTGAGATCCCGAGTCCCGACATGGAGGTGATCTGCAAGAGCTGCATCA 571
Db 210 TCAGGATACAGTGAGATCCCGAGTCCCGACATGGAGGTGATCTGCAAGAGCTGCATCA 269
QY 572 GTCAAAACACCGGGGATAAATCTGGATTTCGGGTCGGCGTCAAGGTGAAGATAATACCTA 631
Db 270 GTCAAAACACCGGGGATAAATCTGGATTTCGGGTCGGCGTCAAGGTGAAGATAATACCTA 329
QY 632 AAGAGGAACACTGTAAATGCCAGAACGAGGTGAAGAGCAACCAAGTTTAAATGAAGA 691
Db 330 AAGAGGAACACTGTAAATGCCAGAACGAGGTGAAGAGCAACCAAGTTTAAATGAAGA 389
QY 692 CAAGCTGAAACCAACGCAAGCTGTTTATATTAGATATTTGACTTAAACTATCTCAATAA 751
Db 390 CAAGCTGAAACCAACGCAAGCTGTTTATATTAGATATTTGACTTAAACTATCTCAATAA 449
QY 752 AGTTTTCG 759
Db 450 AGTTTTCG 457
RESULT 6
AAF68852
ID AAF68852 standard; cDNA; 461 BP.
XX
AC AAF68852;
XX
DT 12-APR-2001 (first entry)
XX
DE Human lung tumour protein related nucleotide sequence SEQ ID NO:792.
XX
KW Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
KW lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
KW cytostatic; antisense inhibition; ss.
XX
OS Homo sapiens.
XX
PN WO200100828-A2.
XX
PD 04-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US18061.
XX
PR 30-JUN-1999; 99US-0346492.
PR 15-OCT-1999; 99US-0419356.
PR 17-DEC-1999; 99US-0466867.
PR 30-DEC-1999; 99US-0476300.
PR 06-MAR-2000; 2000US-0519642.
PR

```
PR 22-MAR-2000; 2000US-0533077.
PR 10-APR-2000; 2000US-0546259.
PR 27-APR-2000; 2000US-0560406.
PR 05-JUN-2000; 2000US-0589184.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
PI Retter MW, Mannion J;
XX
XX WPI: 2001-071488/08.
XX
XX Lung tumor-associated proteins and the nucleic acids that encode them,
XX useful for preventing, diagnosing and treating lung cancer -
XX
XX Claim 4; Page 413; 436pp; English.
XX
XX The present invention describes immunogenic portions of lung tumour-
XX associated proteins (I) and the nucleic acids (NAs) that encode them.
XX (I) have cytostatic activity and can be used in gene therapy, antisense
XX inhibition and in vaccines. The NAs and the lung tumour-associated
XX proteins they encode may be used in the prevention, treatment and
XX diagnosis of diseases associated with their inappropriate expression,
XX especially lung cancers. For example, the NAs may be administered to
XX treat diseases by rectifying mutations or deletions in a patient's genome
XX that affect the activity of the protein by expressing inactive proteins
XX or to supplement the patients own production of (I). Additionally, the
XX NAs may be used to produce the lung-tumour associated protein, according
XX to standard recombinant DNA methodology. Conversely, antisense NA
XX molecules may be administered to down regulate protein expression by
XX binding with the cells own genes and preventing their expression. The NA
XX and complementary sequences may also be used as DNA probes in diagnostic
XX assays to detect and quantitate the presence of similar NA sequences in
XX samples, and hence which patients may be in need of treatment for lung
XX cancer. The (I) may be used as antigens in the production of antibodies
XX and in assays to identify modulators (agonists and antagonists) of the
XX expression and activity of the protein. AAF68083 to AAF68878 and
XX AAB76848 to AAB76878 represent human lung tumour protein related
XX nucleotide and protein sequences which are used in the exemplification
XX of the present invention.
XX
XX Sequence 461 BP; 150 A; 104 C; 123 G; 84 T; 0 other;
XX
XX Query Match 29.7%; Score 232; DB 22; Length 461;
XX Best Local Similarity 100.0%; Pred. No. 2e-98;
XX Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 535 TCGCGCACATGGAAGGTGATCTGCAAGAGCTGCATCAAGTCAAAACACGCGGATAAATCTG 594
XX Db 230 TCGCGCACATGGAAGGTGATCTGCAAGAGCTGCATCAAGTCAAAACACGCGGATAAATCTG 289
XX
XX QY 595 GATTTGGTTCGCGCTCAAGTGAAGATATACCTAAAGAGGAACTGTAAATGCCA 654
XX Db 290 GATTTGGTTCGCGCTCAAGTGAAGATATACCTAAAGAGGAACTGTAAATGCCA 349
XX
XX QY 655 GAAGCAGGTGAAGAGCAACCACTTTAATGAAGACAAGCTGAAACACCGCAAGCTGG 714
XX Db 350 GAAGCAGGTGAAGAGCAACCACTTTAATGAAGACAAGCTGAAACACCGCAAGCTGG 409
XX
XX QY 715 TTTTATTAGATATTGACTTAACCTATCTCAATAAAGTTTTCAGCTTTC 766
XX Db 410 TTTTATTAGATATTGACTTAACCTATCTCAATAAAGTTTTCAGCTTTC 461
XX
XX RESULT 7
XX AAF68152
XX ID AAF68152 standard; cDNA; 479 BP.
XX AC AAF68152;
XX
XX DT 12-APR-2001 (first entry)
XX
XX DE Human lung tumour protein related nucleotide sequence SEQ ID NO:70.
```

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XX
XX KW Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
XX lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
XX KW cytostatic; antisense inhibition; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200100828-A2.
XX
XX PD 04-JAN-2001.
XX
XX PF 30-JUN-2000; 2000WO-US18061.
XX
XX PR 30-JUN-1999; 99US-0346492.
XX PR 15-OCT-1999; 99US-0419356.
XX PR 17-DEC-1999; 99US-0466867.
XX PR 30-DEC-1999; 99US-0476300.
XX PR 06-MAR-2000; 2000US-0519642.
XX PR 22-MAR-2000; 2000US-0533077.
XX PR 10-APR-2000; 2000US-0546259.
XX PR 27-APR-2000; 2000US-0560406.
XX PR 05-JUN-2000; 2000US-0589184.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
PI Retter MW, Mannion J;
XX
XX WPI: 2001-071488/08.
XX
XX Lung tumor-associated proteins and the nucleic acids that encode them,
XX useful for preventing, diagnosing and treating lung cancer -
XX
XX Claim 4; Page 174; 436pp; English.
XX
XX The present invention describes immunogenic portions of lung tumour-
XX associated proteins (I) and the nucleic acids (NAs) that encode them.
XX (I) have cytostatic activity and can be used in gene therapy, antisense
XX inhibition and in vaccines. The NAs and the lung tumour-associated
XX proteins they encode may be used in the prevention, treatment and
XX diagnosis of diseases associated with their inappropriate expression,
XX especially lung cancers. For example, the NAs may be administered to
XX treat diseases by rectifying mutations or deletions in a patient's genome
XX that affect the activity of the protein by expressing inactive proteins
XX or to supplement the patients own production of (I). Additionally, the
XX NAs may be used to produce the lung-tumour associated protein, according
XX to standard recombinant DNA methodology. Conversely, antisense NA
XX molecules may be administered to down regulate protein expression by
XX binding with the cells own genes and preventing their expression. The NA
XX and complementary sequences may also be used as DNA probes in diagnostic
XX assays to detect and quantitate the presence of similar NA sequences in
XX samples, and hence which patients may be in need of treatment for lung
XX cancer. The (I) may be used as antigens in the production of antibodies
XX and in assays to identify modulators (agonists and antagonists) of the
XX expression and activity of the protein. AAF68083 to AAF68878 and
XX AAB76848 to AAB76878 represent human lung tumour protein related
XX nucleotide and protein sequences which are used in the exemplification
XX of the present invention.
XX
XX Sequence 479 BP; 163 A; 107 C; 125 G; 84 T; 0 other;
XX
XX Query Match 24.5%; Score 191; DB 22; Length 479;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-79;
XX Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 535 TCGCGCACATGGAAGGTGATCTGCAAGAGCTGCATCAAGTCAAAACACCGGGGATAATCTG 594
Db 232 TCGCGCACATGGAAGGTGATCTGCAAGAGCTGCATCAAGTCAAAACACCGGGGATAATCTG 291
QY 595 GATTTGGTTCGCGCTCAAGGTGAAGATATACCTAAAGAGGAACTGTAAATGCCA 654
Db 292 GATTTGGTTCGCGCTCAAGGTGAAGATATACCTAAAGAGGAACTGTAAATGCCA 351
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QY 655 GAAGCAGGTGAAGAGCAACACCAAGTTTAAATGAAGACAAAGCTGAACACCAAGCTGG 714
DB 352 GAAGCAGGTGAAGAGCAACACCAAGTTTAAATGAAGACAAAGCTGAACACCAAGCTGG 411
QY 715 TTTTATATTAG 725
DB 412 TTTTATATTAG 422

RESULT 8
AAA42613/c
ID AAA42613 standard; cDNA; 201 BP.
XX
AC AAA42613;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human secreted expressed sequence tag SEQ ID NO:1353.
XX
KW Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST;
KW expressed sequence tag; EST; probe; chemotactic; proliferative;
KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
KW thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
KW antiviral; antidiabetic; antiasthmatic; vulnary; antiparkinsonian;
KW antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic;
KW cerebroprotective; anticonvulsant; antidepressant; gene therapy;
KW vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KW central nervous system disorder; Alzheimer's disease; stroke;
KW parkinson's disease; Huntington's disease; coagulation disorder;
KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
KW tumour; infection; depression; psoriasis; ss.
XX
OS Homo sapiens.
XX
PN WO200021990-A1.
XX
PD 20-APR-2000.
XX
PF 15-OCT-1999; 99WO-US24205.
XX
PR 15-OCT-1998; 98US-0104435.
XX
PA (GENY) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M;
XX
DR WPI; 2000-317937/27.
XX
PT Isolated polynucleotides, and encoded proteins, comprising secreted
PT expressed sequence tags (sESTs), useful for treating various disorders
PT such as autoimmune, infectious, and central nervous system disorders -
XX
XX Claim 1; Page 447; 618pp; English.
XX
XX AAA41261 to AAA43419 represent specifically claimed secreted expressed
CC sequence tags (sESTs), isolated from human, mouse, xenopus and rat
CC tissue sources. The sESTs can have a range of activities depending on
CC the tissues they were isolated from. The activities include:
CC chemotactic; proliferative; immunomodulatory; haematopoietic;
CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
CC antiasthmatic; vulnary; antiulcer; osteopathic; neuroprotective;
CC nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
CC anticonvulsant; and antidepressant. The sESTs can be used for gene
CC therapy and in vaccines. The sESTs are useful as probes for the
CC identification and isolation of full-length cDNAs and genomic DNA
CC molecules which correspond to the sESTs. Proteins encoded by the sESTs
CC are useful in assays for determining biological activity and raising
CC antibodies. They may be useful for treatment of autoimmune disorders
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions

CC (asthma), myeloid or lymphoid cell deficiencies, wounds, ulcers,
CC osteoporosis, osteoarthritis, central nervous system disorders
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
CC disease), tumours, bacterial, fungal or viral infections, depression and
CC psoriasis. AAA43420 to AAA43425 represent linker variants which are given
CC in the exemplification of the present invention.
XX
SQ Sequence 201 BP; 33 A; 56 C; 42 G; 70 T; 0 other;
Query Match 22.3%; Score 174; DB 21; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.5e-71;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 538 GGCACATGGAAGGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAATCTGGAT 597
DB 194 GGCACATGGAAGGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAATCTGGAT 135
QY 598 TTGGGTTCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACACTGTAAAATGCCAGAA 657
DB 134 TTGGGTTCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACACTGTAAAATGCCAGAA 75
QY 658 GCAGGTGAAGAGCAACCAACGCTTTAAATGAAGACAAAGCTGAACACCAAGC 711
DB 74 GCAGGTGAAGAGCAACCAACGCTTTAAATGAAGACAAAGCTGAACACCAAGC 21

RESULT 9
AAL22641
ID AAL22641 standard; cDNA; 822 BP.
XX
AC AAL22641;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 15098.
XX
KW Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001WO-US00798.
XX
PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
PI WPI; 2001-451856/48.
XX
DR New peptide useful as a marker for the diagnosis of breast cancer -
PT
XX Claim 1; Page 2729-2730; 3695pp; English.
XX
CC The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic

Qy 582 GCGGATAAATCTGGATTTCGGTTCCGGCTCAAGGTGAAGATAATACCTAAAGAGGAACA 641
Db 111 GGGGATAAATCTGGATTTCGGTTCCGGCTCAAGGTGAAGATAATACCTAAAGAGGAACA 170
Qy 642 CTCTAAATGCCAGACGAGTGAAGACCAACCAAGTTTAAATGAACAGCTGAAA 701
Db 171 CTCTAAATGCCAGACGAGTGAAGACCAACCAAGTTTAAATGAACAGCTGAAA 230
Qy 702 CAACGCAAGCTGTTTTATATTAGATATTGACTTAAACTATCTCAATAAAGTTTTCGAC 761
Db 231 CAACGCAAGCTGTTTTATATTAGATATTGACTTAAACTATCTCAATAAAGTTTTCGAC 290
Qy 762 CTTTCACCA 770
Db 291 CTTTCACCA 299
RESULT 12
AAC10552
ID AAC10552 standard; cDNA; 190 BP.
XX
AC AAC10552;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 14627.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX Homo sapiens.
XX
XX EPI033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX 26-FEB-1999; 99US-0122487.
XX
XX (GEST) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 14627; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
SQ Sequence 190 BP; 52 A; 51 C; 58 G; 24 T; 5 other;
Query Match 11.5%; Score 90; DB 21; Length 190;
Best Local Similarity 100.0%; Pred. No. 4e-32;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 392 GACACACACAAACACAGAACCCACACAGCCAGTCCAGAGCCCACTAATGGAGAGCCCA 451
Db 83 GACACACACAAACACAGAACCCACACAGCCAGTCCAGAGCCCACTAATGGAGAGCCCA 142
Qy 452 AAAAGAAGAACCCAGCAGCTGAAAGTCGGGA 481
Db 143 AAAAGAAGAACCCAGCAGCTGAAAGTCGGGA 172
RESULT 13
AAL13774
ID AAL13774 standard; cDNA; 618 BP.
XX
AC AAL13774;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 6231.
XX
KW Human; breast cancer; cell marker; cytostatic; ss.
XX Homo sapiens.
XX
XX WO200151628-A2.
XX
XX 19-JUL-2001.
XX
XX 10-JAN-2001; 2001WO-US00798.
XX
XX 14-JAN-2000; 2000US-0176077.
XX
XX 14-MAR-2000; 2000US-0189167.
XX
XX 24-MAR-2000; 2000US-0192099.
XX
XX 29-MAR-2000; 2000US-0193480.
XX
XX 15-MAY-2000; 2000US-0205230.
XX
XX 09-JUN-2000; 2000US-0211315.
XX
XX 25-JUL-2000; 2000US-0220534.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
XX
XX WPI; 2001-451856/48.
XX
PT New peptide useful as a marker for the diagnosis of breast cancer -
XX
PS Claim 1; Page 1118; 3695pp; English.
XX
CC The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
SQ Sequence 618 BP; 169 A; 141 C; 144 G; 119 T; 45 other;
Query Match 8.6%; Score 67; DB 22; Length 618;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGCGGAGCTGTGAGCGCGGAGCTGGGTCCCTGAGGCTGGATTCTTCTCCGCTACT 60
Db 65 GCGCGGAGCTGTGAGCGCGGAGCTGGGTCCCTGAGGCTGGATTCTTCTCCGCTACT 124
Qy 61 GAGACAC 67
Db 125 GAGACAC 131

DT 13-FEB-2002 (first entry)
 XX DNA encoding novel human diagnostic protein #5288.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
 KW Homo sapiens.
 OS WO200175067-A2.
 PN 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI WPI: 2001-639362/73.
 XX P-PSDB; ABG05297.
 DR New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 1; SEQ ID NO 5288; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 503 BP; 158 A; 98 C; 121 G; 105 T; 21 other;
 SQ Query Match 3.5%; Score 27; DB 23; Length 503;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 679 GTTAAATGAAGACAGCTGAACAC 705
 DB 390 GTTAAATGAAGACAGCTGAACAC 416
 RESULT 17
 AAI60530
 ID AAI60530 standard; cDNA: 532 BP.
 XX AAI60530;
 AC AAI60530;
 XX 22-OCT-2001 (first entry)
 DT 22-OCT-2001 (first entry)
 XX

DE Human polynucleotide SEQ ID NO 4519.
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.
 XX Homo sapiens.
 OS WO200153312-A1.
 PN 26-JUL-2001.
 XX 26-DEC-2000; 2000WO-US34263.
 XX 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 DR WPI: 2001-442253/47.
 XX P-PSDB; AAM41374.
 DR Novel nucleic acids and polypeptides, useful for treating disorders
 XX such as central nervous system injuries -
 PT Claim 1; SEQ ID NO 4519; 10078pp; English.
 XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX Sequence 532 BP; 154 A; 108 C; 150 G; 120 T; 0 other;
 SQ Query Match 3.5%; Score 27; DB 22; Length 532;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 679 GTTAAATGAAGACAGCTGAACAC 705
 DB 433 GTTAAATGAAGACAGCTGAACAC 459
 RESULT 18
 AAI58744
 ID AAI58744 standard; cDNA: 659 BP.
 XX AAI58744;
 AC AAI58744;

ID	AA569486 standard; cDNA; 661 BP.
XX	
AC	AA569486;
XX	
DT	13-FEB-2002 (first entry)
XX	
DE	DNA encoding novel human diagnostic protein #5290.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.
KW	Homo sapiens.
OS	
XX	
PN	WO200175067-A2.
XX	
PD	11-OCT-2001.
XX	
PX	30-MAR-2001; 2001WO-US08631.
PF	
PR	31-MAR-2000; 2000US-0540217.
PR	23-AUG-2000; 2000US-0649167.
XX	(HYSE-) HYSEQ INC.
PA	
PI	Drmanac RT, Liu C, Tang YT;
XX	
DR	WPI: 2001-639362/73.
DR	P-PSDB; ABG05299.
XX	
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
XX	
PS	Claim 1; SEQ ID NO 5290; 103pp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes.
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AA564197-AA594564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 661 BP; 212 A; 129 C; 158 G; 162 T; 0 other;
XX	
Query Match	3.5%; Score 27; DB 23; Length 661;
Best Local Similarity	100.0%; Pred. No. 0.01;
Matches	27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	679 GTTTAAATGAAGACAAGCTGAACAAC 705
Db	563 GTTTAAATGAAGACAAGCTGAACAAC 589
RESULT 20	
AAS38132	
ID	AAS38132 standard; cDNA; 391 BP.
XX	

XX	
DT	22-OCT-2001 (first entry)
XX	
DE	Human polynucleotide SEQ ID NO 947.
XX	
KW	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW	peripheral nervous system; neuropathy; central nervous system; CNS;
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW	chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW	leukemia; ss.
OS	
XX	
PN	Homo sapiens.
XX	
PD	WO200153312-A1.
XX	
PX	26-JUL-2001.
PF	
PR	26-DEC-2000; 2000WO-US34263.
PR	21-JAN-2000; 2000US-0489725.
PR	25-APR-2000; 2000US-0552317.
PR	09-JUL-2000; 2000US-0598042.
PR	19-JUL-2000; 2000US-0620312.
PR	03-AUG-2000; 2000US-0653450.
PR	14-SEP-2000; 2000US-0662191.
PR	19-OCT-2000; 2000US-0693036.
PR	29-NOV-2000; 2000US-0727344.
XX	(HYSE-) HYSEQ INC.
PA	
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI	Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX	
DR	WPI: 2001-442253/47.
DR	P-PSDB; AAM39588.
XX	
PT	Novel nucleic acids and polypeptides, useful for treating disorders
PT	such as central nervous system injuries -
XX	
PS	Claim 1; SEQ ID NO 947; 10078pp; English.
XX	
CC	The invention relates to human nucleic acids (AA157798-AA161369) and
CC	the encoded polypeptides (AAM38642-AAAM42213) with nootropic,
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful
CC	in gene therapy. A composition containing a polypeptide or polynucleotide
CC	of the invention may be used to treat diseases of the peripheral nervous
CC	system, such as peripheral nervous injuries, peripheral neuropathy and
CC	localised neuropathies and central nervous system diseases, such as
CC	Alzheimer's Parkinson's disease, Huntington's disease, amyotrophic
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC	utilisation of the activities such as: Immune system suppression,
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC	assays for receptor activity, arthritis and inflammation, leukaemias and
CC	C.N.S disorders.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification.
XX	
SQ	Sequence 659 BP; 197 A; 137 C; 173 G; 152 T; 0 other;
XX	
Query Match	3.5%; Score 27; DB 22; Length 659;
Best Local Similarity	100.0%; Pred. No. 0.01;
Matches	27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	679 GTTTAAATGAAGACAAGCTGAACAAC 705
Db	555 GTTTAAATGAAGACAAGCTGAACAAC 581
RESULT 19	
AA569486	

Thu Oct 17 09:19:16 2002

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AC AAS38132;
XX
DT 17-DEC-2001 (first entry)
XX
DE Novel human diagnostic and therapeutic gene #1190.
XX
XX Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss.
XX
XX Homo sapiens.
XX
XX WO20016753-A2.
XX
XX 13-SEP-2001.
XX
XX 09-MAR-2001; 2001WO-US07787.
XX
XX 09-MAR-2000; 2000US-0188609.
XX
XX (CHIR ) CHIRON CORP.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Randazzo F, Kennedy CC, Pot D, Kassam A, Lamson G;
PI Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX
XX WPI; 2001-530177/58.
XX
XX New polynucleotides and polypeptides, useful for diagnosis and
PT treatment of breast, lung and colon cancer -
XX
XX Claim 1; Page 895; 1193pp; English.
XX
XX The invention relates to new polynucleotides and polypeptides, useful for
CC diagnosis and treatment of breast, lung and colon cancer. The sequences
CC can be used in detecting differentially expressed genes correlated with a
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample derived from a
CC cell suspected of being cancerous. They can also be used to inhibit
CC tumour growth by modulating expression of a gene product. AAS36943-
CC AAS39338 represent novel human diagnostic and therapeutic coding
XX sequences of the invention.
XX
XX Sequence 391 BP; 82 A; 109 C; 117 G; 83 T; 0 other;
SQ
Query Match 3.1%; Score 24; DB 22; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 AGTGAGAGGCCCTCGAAGTCGTC 192
DB 169 AGTGAGAGGCCCTCGAAGTCGTC 192
|||||
RESULT 21
AAS24637
ID AAS24637 standard; cDNA; 214 BP.
XX
XX AAS24637;
AC AAS24637;
XX
XX 07-NOV-2001 (first entry)
DT
DE Human ovarian PCR-subtracted cDNA library clone #818.
XX
XX Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss;
KW gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
KW primer; probe.
XX
XX Homo sapiens.
XX
XX WO200157207-A2.
PN
XX 09-AUG-2001.
XX

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XX 05-FEB-2001; 2001WO-US03733.
XX
XX 04-FEB-2000; 2000US-0180403.
PR
XX 28-MAR-2000; 2000US-0192745.
XX
XX (CORI-) CORIXA CORP.
XX
XX Algate PA, Mannion J;
PI
XX
XX WPI; 2001-488879/53.
XX
XX New polynucleotides encoding ovarian tumour proteins, useful for
PT treating ovarian cancer, and as probes, primers, and markers of cancer
PT progression -
XX
XX Example 1; page 241-242; 378pp; English.
XX
XX The invention comprises compositions used for the therapy and diagnosis
CC of ovarian cancer. The compositions comprise one or more ovarian tumour
CC proteins, their associated polynucleotides, or immunogenic portions of
CC the proteins. The ovarian tumour polynucleotides and polypeptides are
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein. They are also useful for inhibiting the development of cancer in
CC a patient with an ovarian tumour DNA or protein by incubating isolated
CC T-cells allowing them to proliferate, and administering to the patient.
CC The sequences can be used as markers for cancer, for example, to monitor
CC ovarian cancer progression. Probes and primers are useful in nucleic acid
CC hybridisation, in detecting the presence of complementary sequences in a
CC given sample, for preparing mutant species and for preparing other
CC genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS25549
CC represent human ovarian tumour protein cDNA clones.
XX
XX Sequence 214 BP; 74 A; 34 C; 55 G; 51 T; 0 other;
SQ
Query Match 2.9%; Score 23; DB 22; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 645 TAAATGCCAGAGCAGGTGAAG 667
DB 122 TAAATGCCAGAGCAGGTGAAG 144
|||||
RESULT 22
AAH83260
ID AAH83260 standard; cDNA; 320 BP.
XX
XX AAH83260;
AC
XX
XX 25-SEP-2001 (first entry)
DT
DE Human ovarian tumour associated polynucleotide sequence SEQ ID NO:884.
XX
XX Human; ovarian tumour; ovarian cancer; diagnosis; gene therapy;
KW immunogenic; vaccine; ss.
XX
XX Homo sapiens.
XX
XX WO200151513-A2.
PN
XX
XX 19-JUL-2001.
PD
XX
XX 16-JAN-2001; 2001WO-US01575.
XX
XX 14-JAN-2000; 2000US-0176722.
PR
XX
XX (CORI-) CORIXA CORP.
XX
XX Algate PA;
PI
XX
XX WPI; 2001-425866/45.
XX

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PT Novel ovarian tumor proteins, and nucleic acids encoding them, used to
PT treat and diagnose cancers, particularly ovarian cancer .
PS Claim 5; Page 225; 338pp; English.
XX
CC AAH82377 to AAH83878 represent human ovarian tumour-associated
CC polynucleotide sequences which encode ovarian tumour proteins. The
CC ovarian tumour protein and polynucleotide sequences have cytostatic
CC activity, and can be used in gene therapy and vaccine production. The
CC ovarian tumour proteins and polynucleotides can be used to inhibit
CC the development of cancer, particularly ovarian cancer. They can also
CC be used to diagnose the onset and progression of cancer.
XX
SQ Sequence 320 BP; 96 A; 65 C; 85 G; 74 T; 0 other;
Query Match 2.9%; Score 23; DB 22; Length 320;
Best Local Similarity 100.0%; Pred. No. 0.75; Mismatches 0; Gaps 0;
Matches 23; Conservative 0; Indels 0; Gaps 0;
QY 645 TAAATGCCAGAGCAGGTGAAG 667
Db 122 TAAATGCCAGAGCAGGTGAAG 144
RESULT 23
AAF59637
ID AAF59637 standard; cDNA: 580 BP.
AC AAF59637;
XX
XX 24-APR-2001 (first entry)
DT
XX Human cell cycle and proliferation protein CCYPR-48 cDNA, SEQ ID NO:102.
DE
XX Cell cycle and proliferation protein; CCYPR; human; agonist;
KW antagonist; gene therapy; detection; gene therapy;
KW transgenic animal disease model; immune disorder;
KW developmental disorder; cell signalling disorder;
KW cell proliferative disorder; cancer; tumour; anaemia; epilepsy;
KW arteriosclerosis; asthma; allergy; diabetes mellitus;
KW menstrual cycle disorder; bacterial infection; ss.
XX Homo sapiens.
OS
XX WO200107471-A2.
PN
XX 01-FEB-2001.
PD
XX 21-JUL-2000; 2000WO-US19948.
PF
XX 21-JUL-1999; 99US-0145075.
PR
XX 08-SEP-1999; 99US-0153129.
PR
XX 10-NOV-1999; 99US-0164647.
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX Hillman JL, Lal P, Tang YT, Yue H, Au-Young J, Bandman O;
PI Azimzai Y, Yang J, Lu DAM, Baughn MR, Patterson C, Shah P;
XX WPI: 2001-112727/12.
DR
XX P-PSDB; AAB60500.
XX
XX Human cell cycle and proliferation proteins and polynucleotides are
PT used to treat, diagnose and prevent immune, developmental and cell
PT signalling disorders and cell proliferative disorders including cancer .
XX
XX Claim 5; Page 200; 205pp; English.
XX
XX Sequences AAF59590-AAF59643 represent cDNAs encoding 54 human
CC cell cycle and proliferation proteins (CCYPR), AAB60453-AAB60506.
CC CCYPR and agonists of CCYPR are used to treat diseases or conditions
CC associated with decreased expression of functional CCYPR, while CCYPR
CC antagonists are used to treat diseases or conditions associated with

CC overexpression of functional CCYPR. Monoclonal or polyclonal antibodies
CC to CCYPR may be used in enzyme-linked immunosorbent assays (ELISA) or
CC radioimmunoassays to detect CCYPR. CCYPR itself may be used to detect
CC compounds e.g., antibodies, oligonucleotides and proteins (receptors)
CC that specifically bind to CCYPR, and in drug screening methods to
CC identify compounds that modulate the activity of CCYPR. CCYPR
CC nucleotides can be used to generate transgenic animal models of human
CC disease, and can be used in gene therapy in target cells with genetic
CC abnormalities with respect to the expression of CCYPR for the
CC treatment or prevention of a disorder associated with CCYPR.
CC Diseases which can be diagnosed, treated and prevented using CCYPR
CC proteins, nucleic acids, agonists or antagonists include immune,
CC developmental and cell signalling disorders, and cell proliferative
CC disorders including cancer. Specific examples of these disorders
CC include anaemia, epilepsy, arteriosclerosis, asthma, cancer, allergies,
CC diabetes mellitus, disorders of the menstrual cycle and infections
CC caused by bacteria.
XX
SQ Sequence 580 BP; 167 A; 135 C; 160 G; 118 T; 0 other;
Query Match 2.9%; Score 23; DB 22; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.74; Mismatches 0; Gaps 0;
Matches 23; Conservative 0; Indels 0; Gaps 0;
QY 645 TAAATGCCAGAGCAGGTGAAG 667
Db 520 TAAATGCCAGAGCAGGTGAAG 542
RESULT 24
AAD14983
ID AAD14983 standard; DNA: 611 BP.
AC AAD14983;
XX
XX 01-NOV-2001 (first entry)
DT
XX Human NOV4 INA.
DE
XX Human; NOV4; G-antigen; GAGE-like protein; Interferon;
KW G-protein coupled receptor; GPCR; hepatocyte nuclear factor;
KW mast cell protease; gene therapy; proliferative disorder; cancer;
KW immune disorder; hepatic disorder; cirrhosis; viral infection;
KW hepatitis; neuroofactory system-related disorder; neurological disorder;
KW Parkinson's disease; infertility; autoimmune disease; arthritis;
KW multiple sclerosis; allergy; wound healing; cytostatic; nootropic;
KW immunosuppressive; neuroprotective; vulnery; hepatotropic; ds.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 1..173
FT 5'UTR /*tag= a
FT CDS 174..521
FT /*tag= b
FT /*product= "Human NOV4 protein"
FT 3'UTR 522..611
FT /*tag= c
XX WO200161009-A2.
XX
XX 23-AUG-2001.
PD
XX 15-FEB-2001; 2001WO-US04828.
PF
XX 15-FEB-2000; 2000US-0182723.
PR 15-FEB-2000; 2000US-0182724.
PR 15-FEB-2000; 2000US-0182733.
PR 22-FEB-2000; 2000US-0183896.
PR 23-FEB-2000; 2000US-0184275.
PR 23-FEB-2000; 2000US-0184482.
PR 23-FEB-2000; 2000US-0184497.
PR 24-FEB-2000; 2000US-0184744.

PR 13-APR-2000; 2000US-0197083.
PR 10-AUG-2000; 2000US-0224157.
PR 18-SEP-2000; 2000US-0233405.
PR 27-SEP-2000; 2000US-0236060.
PR 02-JAN-2001; 2001US-0259414.
PR 18-JAN-2001; 2001US-0262454.
PR 14-FEB-2001; 2001US-0783429.
XX (CURA-) CURAGEN CORP.
PA Malyankar UM, Tchernev VT, Padigar M, Taupier RJ, Spytek KA;
XX Majumder K, Guo X, Spaderna SK, Boldog FL;
PI WPI; 2001-514775/56.
DR P-PSDB; AAE08583.
XX
XX Isolated novel polypeptides useful for diagnosis of and treating
XX cancer, infertility, autoimmune diseases, arthritis, multiple
XX sclerosis, allergies, wound healing and hepatic disorders -
XX
XX Claim 9; Page 14; 140pp; English.
XX The present sequence is a human NOV4 DNA. The NOVX protein has homology
XX with one of G-antigen (GAGE)-like protein, interferon, G-protein coupled
XX receptor (GPCR), hepatocyte nuclear factor or mast cell protease. The
XX NOVX is useful for treating or preventing a pathology associated with
XX NOVX. It is also useful for determining the presence or amount of NOVX
XX DNA in a sample, for identifying a potential therapeutic agent and in
XX gene therapy. It is also useful for determining the presence of or
XX predisposition to a disease associated with altered levels of NOVX. It is
XX also useful for the diagnosis and treatment of proliferative disorders,
XX e.g., cancer, immune disorders, hepatic disorders, e.g., cirrhosis, viral
XX infections, e.g., hepatitis, neuroendocrine system-related disorders,
XX neurological disorders, e.g., Parkinson's disease, infertility,
XX autoimmune diseases, arthritis, multiple sclerosis, allergies and wound
XX healing.
XX Sequence 611 BP; 196 A; 127 C; 152 G; 135 T; 1 other;
SQ
Query Match 2.9%; Score 23; DB 22; Length 611;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 645 TAAATGCCAGAGCAGGTGAAG 667
DB 472 TAAATGCCAGAGCAGGTGAAG 494
RESULT 25
AAK52902/c
ID AAK52902 standard; cDNA; 665 BP.
XX
XX AAK52902;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 2431.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation; ss.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
XX
XX 27-APR-2000; 2000US-0560875.
XX
XX 20-JUN-2000; 2000US-0598075.
PR

PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
DR P-PSDB; AAM79769.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy -
XX
XX Claim 1; Page 4711; 6221pp; English.
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAM80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX
XX Sequence 665 BP; 156 A; 170 C; 139 G; 200 T; 0 other;
SQ
Query Match 2.9%; Score 23; DB 22; Length 665;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 645 TAAATGCCAGAGCAGGTGAAG 667
DB 142 TAAATGCCAGAGCAGGTGAAG 120
RESULT 26
AAK51918
ID AAK51918 standard; cDNA; 673 BP.
XX
XX AAK51918;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 463.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation; ss.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
XX
XX 27-APR-2000; 2000US-0560875.
XX
XX 20-JUN-2000; 2000US-0598075.
PR

PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX (HYSE-) HYSEQ INC.
PA
XX
XX
PI Zhao YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
DR P-PSDB; AAM78785.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
XX Claim 1; Page 1680-1681; 622lpp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM60020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX Sequence 673 BP; 203 A; 145 C; 170 G; 155 T; 0 other;
XX
XX
XX Query Match 2.9%; Score 23; DB 22; Length 673;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 645 TAAATGCCAGACAGGTGAAG 667
Db 536 TAAATGCCAGACAGGTGAAG 558
XXXXXXXXXXXXXXXXXXXX
RESULT 27
ABL11924/c
ID ABL11924 standard; cDNA; 4652 BP.
XX
XX ABL11924;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ.ID NO 30254.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
KW
KW Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
PR
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI: 2001-656860/75.
DR P-PSDB; ABB67821.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 30254; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 4652 BP; 1051 A; 1138 C; 1165 G; 1298 T; 0 other;
SQ
XX Query Match 2.7%; Score 21; DB 23; Length 4652;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 393 ACACACACAAACACAGAACCA 413
Db 3904 ACACACACAAACACAGAACCA 3884
XXXXXXXXXXXXXXXXXXXX
RESULT 28
AAQ66926/c
ID AAQ66926 standard; DNA; 83 BP.
XX
XX AAQ66926;
XX
XX 25-JAN-1995 (first entry)
XX
XX PolydA detection probe containing flourophores.
DE
XX Target sequence; binding ability; hairpin forming; probes;
KW imperfect hairpin; acceptor label moiety; donor moiety label;
KW fluorescence; fluorophores; specificity; base pair mismatches;
KW competitive arms; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a "Three-site aminoalkyl-derivatised
FT /*note= oligonucleotide with a 6-carbon linker arm
FT attached to an additional fluorophore molecule"
FT stem_loop 1..41
FT /*tag= b
FT /*note= "Forms imperfect hairpin with the competitive
FT arm containing 4 mismatches"
FT misc_difference 42
FT /*tag= c
FT /*note= "6-carbon molecular linker containing a
FT fluorescein molecule and occupying the same
FT space as a base"
FT stem_loop 43..83
FT /*tag= d
FT /*note= "Forms imperfect hairpin with the competitive
FT arm containing 4 mismatches"
FT modified_base 83
FT /*tag= e
FT /*note= "Three-site aminoalkyl-derivatised
FT oligonucleotide with a 6-carbon linker arm

[illegible]

29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0238802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-541565/60.
XX
PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,

useful for preventing, diagnosing and/or treating nervous system cancers and metastases .
PT
XX
PS Disclosure; SEQ ID NO 10259; 1701pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABAI1004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, and ulcerative disease, multiple sclerosis, rheumatoid arthritis and ischaemic colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 21082 BP; 6131 A; 4248 C; 4392 G; 6311 T; 0 other;
Query Match 2.6%; Score 20; DB 22; Length 21082;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 762 CTTTCACCAAAAAAAAAAAAA 781
Db 2635 CTTTCACCAAAAAAAAAAAAA 2654
RESULT 30
ABAI1927
ID ABAI1927 standard; DNA; 21087 BP.
XX
AC ABAI1927;
XX
XX 23-JAN-2002 (first entry)
XX Human nervous system related polynucleotide SEQ ID NO 10258.
XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
OS Homo sapiens.
XX
XX WO2001S9063-A2.
PN
XX 16-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US01334.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0226869.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-02321968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239035.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.

PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2000US-0254097.
PR 05-JAN-2001; 2000US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.

Disclosure; SEQ ID NO 10258; 1701pp + Sequence Listing; English.

The invention relates to novel genes (AB11004-ABA21534) and proteins (AB114678-AB118001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune

CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 21087 BP; 6131 A; 4253 C; 4393 G; 6310 T; 0 other;
Query Match 2.6%; Score 20; DB 22; Length 21087;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 762 CTTTCACCAAAAAA 781
|||||
Db 2635 CTTTCACCAAAAAA 2654
RESULT 31
AAS88056
ID AAS88056 standard; cDNA; 372 BP.
XX
XX
AC AAS88056;
XX
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #23860.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
KW
XX Homo sapiens.
OS
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639367/73.
XX P-PSDB; ABG23869.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 1; SEQ ID No 23860; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 372 BP; 126 A; 76 C; 82 G; 88 T; 0 other;
Query Match 2.4%; Score 19; DB 23; Length 372;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 763 TTTTCACCAAAAAA 781
|||||
Db 347 TTTTCACCAAAAAA 365
RESULT 32
AAK63150/c
ID AAK63150 standard; cDNA; 513 BP.
XX
XX
AC AAK63150;
XX
XX
DT 06-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:8210.
DE
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ss.
KW
XX Homo sapiens.
OS
XX WO200157182-A2.
XX
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN 2000; 2000US 0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 11-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226868.

PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0233397.
 PR 14-SEP-2000; 2000US-0233398.
 PR 14-SEP-2000; 2000US-0233399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 17-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.

PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249254.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 06-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 PI
 XX WPI; 2001-483426/52.
 DR P-PSDB; AAK90369.
 DR
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 PT
 XX Claim 1; SEQ ID NO 8210; 3071pp + Sequence Listing; English.
 PS
 XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 513 BP; 155 A; 87 C; 138 G; 127 T; 6 other;

Query Match 2.4%; Score 19; DB 22; Length 513;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 763 TTTCACCAAAAAAAAAA 781
 DB 20 TTTCACCAAAAAAAAAA 2

```

RESULT 33
AAZ80590/c
ID AAZ80590 standard; cDNA; 705 BP.
XX
XX AC AAZ80590;
XX
XX DT 07-APR-2000 (first entry)
XX
XX DE Human colon cancer cell line SW480 cDNA clone SEQ ID NO:674.
XX
XX KW Human; gene expression product; diagnosis; tumour; colon cancer;
XX colorectal adenocarcinoma; cell line SW480; cell proliferation;
XX cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;
XX hyperplasia; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO9964576-A2.
XX
XX PD 16-DEC-1999.
XX
XX PF 09-JUN-1999; 99WO-IB01062.
XX
XX PR 10-JUN-1998; 98US-0088801.
XX
XX PA (FARB ) BAYER CORP.
XX
XX PI Endege WO, Steinmann KE, Astle JH, Burgess CC, Bushnell SE;
XX Carroll E, Catino TJ, Derti A, Ford DM, Lewis ME, Monahan JE;
XX Schlegel R;
XX
XX DR WPI; 2000-087220/07.
XX
XX PT Novel nucleic acids, used to develop products for the diagnosis and
XX treatment of disorders involving unwanted cell proliferation,
XX particularly cancers, especially colon cancer -
XX
XX PS Claim 15; Page 399; 469pp; English.
XX
XX CC AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from
XX the human colorectal adenocarcinoma (colon cancer) cell line SW480. The
XX cDNA clones can be used to generate antisense oligonucleotides which
XX can be used for antisense therapy. Methods and products from the present
XX invention can be used for identifying and/or classifying cancerous cells
XX present in a human tumour, particularly in solid tumours, e.g.
XX carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones
XX can be used for developing agents for the diagnosis and treatment of
XX disorders involving unwanted cell proliferation, such as neoplasia,
XX dysplasia or hyperplasia.
XX
XX SQ Sequence 705 BP; 144 A; 157 C; 166 G; 213 T; 25 other:
XX
XX Query Match 2.4%; Score 19; DB 21; Length 705;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 763 TTTCACCAAAAAAAAAAAAA 781
Db 37 TTTCACCAAAAAAAAAAAAA 19

RESULT 34
AAQ32851/c
ID AAQ32851 standard; cDNA; 1547 BP.
XX
XX AC AAQ32851;
XX
XX DT 05-MAY-1993 (first entry)
XX
XX DE BMP2.
XX
XX KW Bone; morphogenetic; protein; BMP; growth; vitamin D; systemic;
XX treatment; dimer; ss.

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XX
XX OS Rattus rattus.
XX
XX PN WO9221365-A.
XX
XX PD 10-DEC-1992.
XX
XX PF 26-MAY-1992; 92WO-US04356.
XX
XX PR 05-JUN-1991; 91US-0709621.
XX
XX PR 27-MAR-1992; 92US-0856110.
XX
XX PA (PROC ) PROCTER & GAMBLE CO.
XX
XX PI Stone RL;
XX
XX DR WPI; 1992-433371/52.
XX
XX PT Synergistic compsn. for generating mammalian bone growth -
XX comprises vitamin-D cpd. and bone morphogenetic protein
XX
XX PS Disclosure; Page 27-29; 44pp; English.
XX
XX CC The sequences given in AAQ32850-56 encode bone morphogenetic proteins
XX (BMP). BMP's increase bone growth and when used in conjunction with
XX vitamin D the level of new bone growth is greater than when a BMP or
XX vitamin D are used alone. The BMP's are administered for systemic
XX treatment at a dose range of 1pg to 100 microg. BMP are active as
XX dimers.
XX
XX SQ Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 other:
XX
XX Query Match 2.4%; Score 19; DB 13; Length 1547;
XX Best Local Similarity 100.0%; Pred. No. 53;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GGCCGAGGAGTGGAGGGGC 281
Db 119 GGCCGAGGAGTGGAGGGGC 101

RESULT 35
AAV01679/c
ID AAV01679 standard; cDNA; 1547 BP.
XX
XX AC AAV01679;
XX
XX DT 27-MAR-1998 (first entry)
XX
XX DE Bone morphogenetic protein BMP-2 encoding DNA.
XX
XX KW Bone morphogenetic protein; BMP; growth; vitamin D; fracture;
XX arthritis; surgical lesion; periodontal disease; osteoporosis;
XX rickets; ds.
XX
XX OS Unidentified.
XX
XX PN US5693615-A.
XX
XX PD 02-DEC-1997.
XX
XX PF 05-JUN-1991; 91US-0709621.
XX
XX PR 07-SEP-1993; 93US-0117367.
XX
XX PR 05-JUN-1991; 91US-0709621.
XX
XX PR 27-MAR-1992; 92US-0856110.
XX
XX PR 09-DEC-1992; 92US-0988363.
XX
XX PR 13-MAY-1994; 94US-0243435.
XX
XX PR 23-JAN-1995; 95US-0377292.
XX
XX PA (PROC ) PROCTER & GAMBLE CO.
XX
XX PI Stone RL;

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XX WPI: 1998-031788/03.
XX
XX Generation of new bone growth - by co-administering bone
XX morphogenetic protein and vitamin D
XX
XX Claim 1; Column 19-22; 18pp; English.
XX
XX A new method has been developed for generating new bone growth in a
XX mammal. The method comprises administering a bone morphogenetic protein
XX in combination with a vitamin D compound, where: (a) the bone
XX morphogenetic protein is BMP-2 and is administered in an amount of
XX 500-1000 ng in combination with about 6 ng vitamin D compound; or (b)
XX the bone morphogenetic protein is BMP-4 and is administered in an
XX amount of about 62.5 ng in combination with about 6 ng vitamin D
XX compound. The present sequence encodes BMP-2. The method is used for
XX treating bone defects or disorders, e.g. fractures, surgical lesions,
XX periodontal disease, osteoporosis, arthritis and rickets.
XX
XX Sequence 1547 BP; 377 A; 423 C; 410 G; 337 T; 0 other;
SQ
Query Match 2.4%; Score 19; DB 19; Length 1547;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 263 GCGCGAGGAGTGGAGGGGC 281
DB 119 GCGCGAGGAGTGGAGGGGC 101

RESULT 36
AAN80632/c
ID AAN80632 standard; DNA: 1606 BP.
XX
XX AAN80632;
XX
XX 08-OCT-1990 (first entry)
XX
XX Human Bone Morphogenic Protein-2 class I cDNA.
XX
XX Bone morphogenic protein; hBMP-2 class I; probes; cartilage formation;
XX bone formation; osteogenic cpds; prodontal disease; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 356..1543
XX /*tag= a
XX /product=hBMP-2 class I
XX
XX W08800205-A.
XX
XX 14-JAN-1988.
XX
XX 30-JUN-1987; 87WO-0501537.
XX
XX 26-MAR-1987; 87US-0031346.
XX
XX (GENE-) GENETICS INST INC.
XX
XX Wozney JW, Rosen VA;
XX
XX WPI: 1988-021565/03.
XX P-PSDB; AAP80619.
XX
XX Bone morphogenic proteins - obtd. using recombinant DNA and used
XX for inducing cartilage and bone formation.
XX
XX Disclosure; 7pp; English.
XX
XX The HindIII-SacI bovine genomic bBMP-2 fragment described in AAN80627
XX is subcloned into M13, labelled and used as probe to screen
XX polyadenylated RNAs from various cells and tissue sources.
XX

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```

CC Sequence analysis of the strongly hybridising clones hBMP-2 class I
CC (-BMP-2) indicated that they have extensive homology with the sequence
CC given in AAN80622.
CC The partial sequence is compiled from lambda U20S-39 and several
CC other hBMP-2 class I cDNA recombinants.
CC This human cDNA hBMP-2 class I contains an open reading frame of 1188
CC bp, encoding a protein of 396 amino acids. The protein is preceded by a
CC 5' untranslated region of 342 bp with stop codons in all frames. The 13
CC bp region preceding this 5' untranslated region represents a linker used
CC in the cDNA cloning procedures.
CC See also AAN80619-N80636 and AAN81963-64.
XX
XX Sequence 1606 BP; 399 A; 430 C; 423 G; 354 T; 0 other;
SQ
Query Match 2.4%; Score 19; DB 9; Length 1606;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 263 GCGCGAGGAGTGGAGGGGC 281
DB 151 GCGCGAGGAGTGGAGGGGC 133

RESULT 37
AAQ14036/c
ID AAQ14036 standard; DNA: 1607 BP.
XX
XX AAQ14036;
XX
XX 13-JAN-1992 (first entry)
XX
XX Human BMP-2A in lambda U20S-39.
XX
XX Bone; cartilage; osteoinductive protein; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 356..1546
XX /*tag= a
XX Misc_RNA 356..1543
XX /*tag= b
XX /label= claim 1(b)
XX
XX US5013649-A.
XX
XX 07-MAY-1991.
XX
XX 08-APR-1988; 88US-0179100.
XX
XX 01-JUL-1986; 86US-0880776.
XX 04-APR-1988; 88US-0179100.
XX
XX (GENE-) GENETICS INST INC.
XX
XX WPI: 1991-309401/42.
XX P-PSDB; AAR14241.
XX
XX New DNA sequences encoding osteo-inductive protein - useful for
XX stimulating bone and cartilage re formation e.g. for wound healing
XX and tissue repair.
XX
XX Disclosure; Fig 2; 20pp; English.
XX
XX The sequence was obtd. from clone lambda U20S-39 (ATCC 40345)
XX which was isolated from a cDNA library prepd. using human cell line
XX U-2 OS RNA. It is one of two classes of clones isolated
XX distinguished by hybridisation characteristics. This class,
XX designated hBMP-2A (previously BMP-2 and BMP-2 Class I) hybridised
XX strongly with the probe which was derived from the bovine BMP-2A
XX sequence, and showed strong homology with that sequence. The second
XX class, hBMP-2B (previously BMP-4 and BMP-2 Class II) hybridised only
XX weakly and is less homologous, esp. at the 3' end. The gene prod.

```


CC is an osteoinductive protein useful for inducing bone/cartilage
CC repair, wound healing and tissue repair. Typical applications
CC include healing of bone fractures; improved fixation of artificial
CC joints; in cosmetic plastic surgery; and in treatment of periodontal
CC disease, burns, incisions, ulcers etc.
CC See also AAQ14035 and AAQ14037, AAQ14909 and AAQ14910.
XX
SQ Sequence 1607 BP; 400 A; 430 C; 421 G; 356 T; 0 other;

Query Match 2.4%; Score 19; DB 12; Length 1607;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GCCGAGGAGTGAGGGGC 281
Db 151 GCCCAGGAGTGAGGGGC 133

RESULT 38
AAQ31869/c
ID AAQ31869 standard; DNA: 1607 BP.

XX AAQ31869;
XX 16-APR-1993 (first entry)
XX Human BMP-2A sequence.
XX Bone Morphogenic Protein; bacteriophage lambda U2OS-39; ATCC 40345;
KW bone fracture; cartilage defect; osteoporosis; ss.
KW
XX Homo sapiens.

XX Key Location/Qualifiers
FH 356..1546
FT CDS /*tag= a
FT /*product= BMP-2A
FT mat_peptide 1202..1543
FT /*tag= b
FT /*note= "preceded by pre-pro region"

XX US5166058-A.
XX 24-NOV-1992.
XX 11-JUL-1989; 89US-0378537.
XX 01-JUL-1986; 86US-0880776.
XX 17-DEC-1986; 86US-0943332.
XX 20-MAR-1987; 87US-0028285.
XX 08-APR-1988; 88US-0179100.
XX 11-JUL-1989; 89US-0378537.
XX (GEMY) GENETICS INST INC.

XX Rosen VA, Wang EA, Wozney JM;
XX WPI; 1992-414955/50.
XX P-PSDB; AAR29281.
XX DNA encoding osteo-inductive proteins - used for producing BMP-2A
PT and BMP-2B for inducing bone or cartilage formation and wound
PT healing
XX

PS Claim 1; Fig 2; 22pp; English.
XX A human U2OS cDNA library was screened with a bovine BMP-2A probe
CC (see AAQ31868). Sequence analysis of strongly hybridising clones
CC designated hBMP-2A (previously designated BMP-2 and BMP-2 Class I)
CC indicated that they have extensive homology with the partial bovine
CC BMP-2A sequence; weakly hybridising clones were designated hBMP-2B
CC (previously designated BMP-4 and BMP-2 Class II) and sequence
CC analysis indicated these clones were quite homologous with the

CC bovine sequence at their 3' end but less so at the 5' end. A
CC full-length human BMP-2A cDNA clone was obtained by screening the
CC U2OS library with the insert of a BMP-2B subclone.
XX
SQ Sequence 1607 BP; 400 A; 430 C; 422 G; 355 T; 0 other;

Query Match 2.4%; Score 19; DB 13; Length 1607;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GCCCGAGGAGTGAGGGGC 281
Db 151 GCCCGAGGAGTGAGGGGC 133

RESULT 39
AAQ41291/c
ID AAQ41291 standard; DNA: 1607 BP.

XX AAQ41291;
XX 13-SEP-1993 (first entry)
XX Human BMP-2 gene.
XX Bone morphogenetic protein; bone defect treatment; healing; wound;
KW injury; tissue repair; osteoporosis; burns; incisions; ulcers;
KW neuronal survival increase; fracture reduction; cartilage growth;
KW induction; ss.
XX Homo sapiens.

XX Key Location/Qualifiers
FH 356..1543
FT CDS /*tag= a
FT
XX WO9309229-A.
XX 13-MAY-1993.
XX 02-NOV-1992; 92WO-US09430.
XX 04-NOV-1991; 91US-0787496.
XX 07-APR-1992; 92US-0864692.

XX (GEMY) GENETICS INST INC.
XX Israel D, Wolfman NM;
XX WPI; 1993-167696/20.
XX P-PSDB; AAR36732.
XX Recombinant hetero-dimeric BMP proteins - are useful in treating
PT bone defects, healing bone injury and in wound healing
PT
XX Disclosure; Fig 1; 169pp; English.

XX The sequence is that encoding the human bone morphogenetic protein
CC BMP-2. It may be used in the prodn. of a recombinant heterodimeric
CC protein having bone stimulating activity. This heterodimer is
CC encoded by a sequence encoding BMP-2 or a fragment and a sequence
CC encoding a second protein or fragment selected from BMP-5, BMP-6,
CC BMP-7 or BMP-8. It may be used in compsns. for wound healing, tissue
CC repair, and in similar compsns. which have been indicated for the
CC use of individual BMPs. Increased potency of the heterodimer over
CC individual BMPs may permit lower dosages to be administered. A
CC heterodimeric protein which induces cartilage and/or bone growth
CC in circumstances where bone is not normally formed, has
CC applications in the healing of bone fractures and cartilage defects
CC in humans and other animals. The heterodimer may have prophylactic use
CC in closed as well as open fracture reduction and also in the
CC improved fixation of artificial joints. De novo bone formation
CC induced by an osteogenic agent contributes to the repair of

CC congenital, trauma induced or oncologic resection induced craniofacial
CC defects, and also is useful in cosmetic plastic surgery. It may be
CC used in the treatment of periodontal disease and in other tooth
CC repair processes. It may also be useful in the treatment of
CC osteoporosis, wound healing (e.g. burns, incisions and ulcers) and
CC related tissue repair, and may increase neuronal survival and be useful
CC in the transplantation and treatment of conditions exhibiting a decrease
CC in neuronal survival. It may be combined with other agents beneficial to
CC the bone and/or cartilage defect, wound or tissue in question, e.g. EGF,
CC PDGF, TGF-alpha, TGF-beta and insulin-like growth factor
XX
SQ Sequence 1607 BP; 400 A; 430 C; 423 G; 354 T; 0 other;

Query Match 2.4%; Score 19; DB 14; Length 1607;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 263 GCCCGAGGAGTGGAGGGGC 281
|||||
Db 151 GCCCGAGGAGTGGAGGGGC 133

RESULT 40
AAT78941/c
ID AAT78941 standard; cDNA; 1607 BP.

XX
AC AAT78941;

XX
DT 22-JAN-1998 (first entry)

XX
DE Human bone morphogenic protein (BMP) 2A cDNA.

XX
KW bone morphogenic protein; BMP 2A; cartilage; periodontal disease;
KW tissue repair; osteoporosis; treatment; oligonucleotide probe; ss.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT 5'UTR 1..355
FT /*tag= a
FT CDS 356..1546
FT /*tag= b
FT misc_feature 356..424
FT /*tag= c
FT misc_feature /note= "pre-portion of BMP-2A"
FT 425..1201
FT /*tag= d
FT mat_peptide 1202..1543
FT /*tag= e
FT 3'UTR /note= "mature portion of BMP-2A"
FT 1547..1607
FT /*tag= f

XX
PN US5631142-A.

XX
PD 20-MAY-1997.

XX
PF 07-SEP-1993; 93US-0118363.

XX
PR 11-JUL-1989; 89US-0378537.

PR 17-DEC-1986; 86US-0943332.

PR 20-MAR-1987; 87US-0028285.

PR 08-APR-1988; 88US-0179100.

PR 18-MAY-1992; 92US-0884353.

PR 07-SEP-1993; 93US-0118363.

PR 01-JUL-1986; 86US-0880776.

XX
PA (GEM) GENETICS INST INC.

XX
PI Rosen VA, Wang EA, Wozney JM;

XX
DR WPI; 1997-288573/26.

DR P-PSDB; AAW24849.

XX
PT Production of human bone morphogenic protein 2A or 2B in cell
PT culture - useful inducing bone or cartilage production, in wound
PT healing and tissue repair

XX
PS Claim 2; Fig 2; 22pp; English.

XX
CC This cDNA sequence encodes the human bone morphogenic protein (BMP) 2A.
CC Oligonucleotide probes were synthesised based on a partially sequenced
CC BMP-2A protein isolated from ground bovine powder. The probes were used
CC to screen a bovine liver DNA library to obtain the BMP-2A encoding DNA
CC sequence. The DNA was used to screen a U-2 OS human cell line cDNA
CC library to obtain this human BMP-2A cDNA. BMPs can be used to induce
CC bone and cartilage formation, and in wound healing and tissue repair.
CC They can also be used for treating periodontal disease or osteoporosis.

SQ Sequence 1607 BP; 400 A; 430 C; 422 G; 355 T; 0 other;

Query Match 2.4%; Score 19; DB 18; Length 1607;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 263 GCCCGAGGAGTGGAGGGGC 281

|||||

Db 151 GCCCGAGGAGTGGAGGGGC 133

Search completed: October 16, 2002, 22:03:13

Job time : 243 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	781	100.0	781	22	AAF68861	Human lung tumour
2	391	50.1	396	22	AAS37109	Novel human diagno
3	391	50.1	762	22	AAH64751	Human secreted pro
4	390.6	50.0	399	22	AAF68151	Human lung tumour
5	369	47.2	457	22	AAF68851	Human lung tumour
6	361.8	46.3	618	22	AAL13774	Human breast cancer
7	356.2	45.6	822	22	AAL22641	Human breast cancer
8	354	45.3	479	22	AAF68152	Human lung tumour
9	350	44.8	461	22	AAF68852	Human lung tumour

10	305	39..1	391	22	AAS38132	Novel human diaphanous GTPase
11	226	28..9	300	20	AA55997	Human cDNA clone F
12	216.4	27..7	659	22	AA158744	Human polynucleotide
13	214.8	27..5	673	22	AAK51918	Human polynucleotide
14	201.8	25..8	611	22	AAAD14983	Human NOV4 DNA, H
15	201.2	25..8	503	23	AA569484	DNA encoding novel
16	197	25..2	208	21	AAAC17098	Human secreted protein
17	195.6	25..0	532	22	AAI160530	Human polynucleotide
18	171.8	22..4	201	21	AAA42613	DNA encoding novel
19	174.8	22..0	661	23	AA569486	Human cell cycle
20	169	21..6	580	22	AAAF59637	Human metastatic
21	163.8	21..0	1092	21	AAK45936	DNA encoding novel
22	142.6	18..3	665	22	AAK52902	Human polynucleotide
23	139.2	17..8	750	23	AAAS91235	DNA encoding novel
24	135	17..3	320	22	AAH83360	Human ovarian tumor
25	133.2	17..1	214	22	AAAS24637	Human ovarian PCR-
26	132.6	17..0	2182	21	AAAS59112	Human secreted protein
27	111.6	14..3	539	19	AAAV18721	DNA encoding GAGE
28	110	14..1	540	20	AAAX90521	GAGE-4 tumour reje
29	110	14..1	540	20	AAAX90523	GAGE-6 tumour reje
30	108.4	13..9	532	19	AAAV18720	DNA encoding GAGE
31	108.4	13..9	532	20	AAAX90522	DNA encoding GAGE
32	108.4	13..9	535	19	AAAV18717	GAGE-2 tumour reje
33	108.4	13..9	538	20	AAAX90519	DNA encoding GAGE
34	108.4	13..9	560	19	AAAV18718	GAGE-3 tumour reje
35	108.4	13..9	560	20	AAAX90520	Human cancer agent
36	108.4	13..9	1245	22	AAAS60826	Human prostate can
37	108.8	13..7	1024	21	AAAZ97217	Human NOV2 DNA, H
38	106.4	13..6	475	22	AAAD14981	Human prostate can
39	105.8	13..5	1024	21	AAAZ97216	Human NOV3 DNA, H
40	103.2	13..2	1051	22	AAAD14982	Human secreted protein
41	102.4	13..1	190	21	AAAC10552	DNA encoding GAGE
42	99	12..7	541	19	AAAV18719	Human cancer agent
43	95.8	12..3	530	22	AAAS60104	Human secreted protein
44	91.4	11..7	571	21	AAAZ33316	Human secreted protein
45	89.6	11..5	472	21	AAAZ95012	CSG Prol18 EST use

RESULT 1

AAAF68861

AAAF68861 standard; cDNA; 781 BP.

AAAF68861;

12-APR-2001 (first entry)

Human lung tumour protein related nucleotide sequence SEQ ID NO:808.

Human; lung cancer; lung tumour; lung tumour protein; gene therapy;

lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;

cytostatic; antisense inhibition; ss.

Homo sapiens.

WO200100828-A2.

04-JAN-2001.

30-JUN-2000; 2000WO-US18061.

30-JUN-1999; 99US-0346492.

15-OCT-1999; 99US-0419356.

17-DEC-1999; 99US-0466867.

30-DEC-1999; 99US-0476300.

06-MAR-2000; 2000US-0519642.

22-MAR-2000; 2000US-0533077.

10-APR-2000; 2000US-0546259.

27-APR-2000; 2000US-0560406.

05-JUN-2000; 2000US-0589184.

(CORI-) CORIXA CORP.
Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedwick TS, Carter D;
Retter MW, Mannion J;
WPI: 2001-071498/08.
Lung tumor-associated proteins and the nucleic acids that encode them,
useful for preventing, diagnosing and treating lung cancer .
Claim 4; Page 426; 436pp; English.
The present invention describes immunogenic portions of lung tumour-
associated proteins (I) and the nucleic acids (NAS) that encode them.
(I) have cytostatic activity and can be used in gene therapy, antisense
inhibition and in vaccines. The NAS and the lung tumour-associated
proteins they encode may be used in the prevention, treatment and
diagnosis of diseases associated with their inappropriate expression,
especially lung cancers. For example, the NAS may be administered to
treat diseases by rectifying mutations or deletions in a patient's genome
that affect the activity of the protein by expressing inactive proteins
or to supplement the patient's own production of (I). Additionally, the
NAS may be used to produce the lung-tumour associated protein, according
to standard recombinant DNA methodology. Conversely, antisense NA
molecules may be administered to down regulate protein expression by
binding with the cells own genes and preventing their expression. The NA
and complementary sequences may also be used as DNA probes in diagnostic
assays to detect and quantitate the presence of similar NA sequences in
samples, and hence which patients may be in need of treatment for lung
cancer. The (I) may be used as antigens in the production of antibodies
and in assays to identify modulators (agonists and antagonists) of the
expression and activity of the protein. AAF68083 to AAF68878 and
AAB76848 to AAB76878 represent human lung tumour protein related
nucleotide and protein sequences which are used in the exemplification
of the present invention.
Sequence 781 BP: 230 A; 181 C; 234 G; 136 T; 0 other;
Query Match 100.0%; Score 781; DB 22; Length 781;
Best Local Similarity 100.0%; Pred. No. 6e-224;
Matches 781; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGCGGAGCTGTGAGCGGGGAGCTCGGCTCCCTGAGGTCTGGATTCTTTCTCCGCTACT 60
Db 1 GCGCGGAGCTGTGAGCGGGGAGCTCGGCTCCCTGAGGTCTGGATTCTTTCTCCGCTACT 60
Qy 61 GAGACACAGCGGGTAGGTCCACAGCGAGATCCAACTGGGAGTTGAAGTGTGAGTGAGAGT 120
Db 61 GAGACACAGCGGGTAGGTCCACAGCGAGATCCAACTGGGAGTTGAAGTGTGAGTGAGAGT 120
Qy 121 GAAGAAGACAGAGGCTTCCGAGGGTGTGTGTCAGTCACTCAGAGTGAGAAGGCC 180
Db 121 GAAGAAGACAGAGGCTTCCGAGGGTGTGTGTCAGTCACTCAGAGTGAGAAGGCC 180
Qy 181 CTCGAAGTCGTCT 240
Db 181 CTCGAAGTCGTCT 240
Qy 241 GCCATAACTAGGAGGAGGAGGCGCCGAGGAGTGGAGGGCTCAGCGCAAGCTCGGGTGC 300
Db 241 GCCATAACTAGGAGGAGGAGGCGCCGAGGAGTGGAGGGCTCAGCGCAAGCTCGGGTGC 300
Qy 301 TGTGGGGGTATCCGAGTCCAGAGCACTTGGAAACCCCGACAGAGATTTCTGACTCC 360
Db 301 TGTGGGGGTATCCGAGTCCAGAGCACTTGGAAACCCCGACAGAGATTTCTGACTCC 360
Qy 361 CAGAGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
Db 361 CAGAGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
Qy 421 ACTCCAGAGCCCAAGTAAGGAGAGGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 AGTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480

Qy 481 ATCTTACACCTGGGCGAGCAGACAGAGAAGATCAGATACAGCTGAGATCCAGTCCCGC 540
Db 481 ATCTTACACCTGGGCGAGCAGACAGAGAAGATCAGATACAGCTGAGATCCAGTCCCGC 540
Qy 541 ACATGGAAGGTCATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATCTGGATTG 600
Db 541 ACATGGAAGGTCATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATCTGGATTG 600
Qy 601 GGTTCGGCGCTCAAGGTGAAGATAATACCTAAAGAGGAACTGTAAATGCGAAGCA 660
Db 601 GGTTCGGCGCTCAAGGTGAAGATAATACCTAAAGAGGAACTGTAAATGCGAAGCA 660
Qy 661 GGTGAAGACCAACACAGTTTAAATGAAGCAAGCTGAAACAGCAAGCTGGTTTAT 720
Db 661 GGTGAAGACCAACACAGTTTAAATGAAGCAAGCTGAAACAGCAAGCTGGTTTAT 720
Qy 721 ATTAGATATTTGACATTAACACTCTCAATAAAGTTTTCAGCTTTCACCAAAAAA 780
Db 721 ATTAGATATTTGACATTAACACTCTCAATAAAGTTTTCAGCTTTCACCAAAAAA 780
Qy 781 A 781
Db 781 A 781
RESULT 2
AAS37109
ID AAS37109 standard; cDNA; 396 BP.
XX AC AAS37109,
XX DT 17-DEC-2001 (first entry)
XX DE ~~NOVEL~~ human diagnostic and therapeutic gene #167.
XX KW Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss.
XX OS Homo sapiens.
XX PN WO200166753-A2.
XX PD 13-SEP-2001.
XX PF 09-MAR-2001; 2001WO-US07782.
XX PR 09-MAR-2000; 2000US-0188609.
XX PA (CHIR) CHIRON CORP.
XX PA (HYSE-) HYSEQ INC.
XX PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Randazzo F, Kennedy GC, Pot D, Kassam A, Lamson G;
PI Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leskowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
XX WPI: 2001-530177/58.
XX New polynucleotides and polypeptides, useful for diagnosis and
treatment of breast, lung and colon cancer -
Claim 1; Page 638; 1193pp; English.
The invention relates to new polynucleotides and polypeptides, useful for
diagnosis and treatment of breast, lung and colon cancer. The sequences
can be used in detecting differentially expressed genes correlated with a
cancerous state of a mammalian cell, comprising detecting at least one
differentially expressed gene product in a test sample derived from a
cell suspected of being cancerous. They can also be used to inhibit
tumour growth by modulating expression of a gene product. AAS36943-
AAS39338 represent novel human diagnostic and therapeutic coding
sequences of the invention.

SQ Sequence 396 BP; 82 A; 97 C; 146 G; 71 T; 0 other;

Query Match 50.1%; Score 391; DB 22; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.2e-107;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGCGGAGCTGTGAGCCGGGACTCGGGTCCCTGAGGCTCTGATTCCTTCTCCGCTACTG 61
DB 1 CGCGGAGCTGTGAGCCGGGACTCGGGTCCCTGAGGCTCTGATTCCTTCTCCGCTACTG 60

QY 62 AGACACGGCGGTAGGTCCACAGGCGAGATCCAACTGGGAGTTGAAGTGTGAGTGTGAGAGTG 121
DB 61 AGACACGGCGGTAGGTCCACAGGCGAGATCCAACTGGGAGTTGAAGTGTGAGTGTGAGAGTG 120

QY 122 AGAGGAACACAGGCTCCCGAGGGTTGTGTGTGCTGAGTCACTCAGAGTGAGAGAGGCC 181
DB 121 AGAGGAACACAGGCTCCCGAGGGTTGTGTGTGCTGAGTCACTCAGAGTGAGAGAGGCC 180

QY 182 TCGAAGTCGTCTCTCTCATGCGGTGCCACGCCCATGGACCTTCTTGTCTCTGTCACGG 241
DB 181 TCGAAGTCGTCTCTCTCATGCGGTGCCACGCCCATGGACCTTCTTGTCTCTGTCACGG 240

QY 242 CCATAACTAGGAGGAAGAGGCGCGGAGGAGTGGAGGGGCTCAGGCGAAGCTGGGGTGCT 301
DB 241 CCATAACTAGGAGGAAGAGGCGCGGAGGAGTGGAGGGGCTCAGGCGAAGCTGGGGTGCT 300

QY 302 GTTGGGGGTATCCGAGTCCACAGACACCTGGAACCCCGACAGAGATTTCTGGACTCCCC 361
DB 301 GTTGGGGGTATCCGAGTCCACAGAGCACCTGGAACCCCGACAGAGATTTCTGGACTCCCC 360

QY 362 AGACGGGACAGGAGAGGGGACGCGCATGAGCG 392
DB 361 AGACGGGACAGGAGAGGGGACGCGCATGAGCG 391

RESULT 3
AAH64751
ID AAH64751 standard; cdna; 762 BP.
XX
AC AAH64751;
XX
DT 11-SEP-2001 (first entry)
XX
DE Human secreted protein cDNA, SEQ ID NO: 27.
XX
KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
KW GENSET; ss.
XX
OS Homo sapiens.
XX
PN WO200142451-A2.
XX
PD 14-JUN-2001.
XX
PF 07-DEC-2000; 2000WO-1B01938.
XX
PR 08-DEC-1999; 99US-0169629.
XX
PR 06-MAR-2000; 2000US-0187470.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Bougueleret L, Jobert S;
XX
XX WPI; 2001-367870/38.
DR P-PSDB; AAG89148.
XX
XX Full length GENSET human nucleic acids encoding potentially secreted
PT proteins, useful in gene therapy and vaccination against a variety of
PT diseases, and for diagnosis of those diseases -
XX
XX Claim 7; Page 586; 921pp; English.
PS
XX The invention relates to full length GENSET human nucleic acids encoding

CC potentially secreted proteins. The nucleic acids and the polypeptides
CC they encode may be used in the prevention, treatment and diagnosis of
CC diseases associated with inappropriate GENSET gene expression. For
CC example, they be used to treat disorders associated with decreased
CC GENSET gene expression by rectifying mutations or deletions in a
CC patient's genome that affect the activity of GENSET or by supplementing
CC the patient's own production of GENSET polypeptides. Conversely,
CC antisense nucleic acid molecules may be administered to down regulate
CC GENSET expression by binding with the cells' own genes and preventing
CC their expression. The sense and antisense nucleic acids may also be
CC used as DNA probes in diagnostic assays to detect and quantitate the
CC presence of similar nucleic acid sequences in samples, and hence to
CC determine which patients may be in need of restorative therapy.
CC The GENSET polypeptides may be used as antigens in the production of
CC antibodies and in assays to identify modulators (agonists and
CC antagonists) of GENSET polypeptide expression and activity. The
CC present sequence is a GENSET nucleic acid of the invention.
XX
SQ Sequence 762 BP; 220 A; 192 C; 186 G; 164 T; 0 other;

Query Match 50.1%; Score 391; DB 22; Length 762;
Best Local Similarity 98.7%; Pred. No. 5.9e-107;
Matches 394; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 383 GGCATGAGCGACACACACAAACACAGAACCCAGTCCCGAGGAGCCAGTAATGG 442
DB 361 GACAGCGCGGACACACACAAACACAGAACCCAGTCCCGAGGAGCCAGTAATGG 420

QY 443 AGAGCCCCAAAGAGAGAACCCAGCAGCTGAAAGTCGGGATCCTACACCTGGCGACGAC 502
DB 421 AGAGCCCCAAAGAGAGAACCCAGCAGCTGAAAGTCGGGATCCTACACCTGGCGACGAC 480

QY 503 AGAAGAAGTACAGGATACAGCTGAGATCCAGTCCCGAGGAGCCAGTGAAGTGTGATCTCAAGA 562
DB 481 AGAA''AGATCAG:ATACAGCTGAGATCCAGTCCCGAGGAGCCAGTGAAGTGTGATCTCAAGA 540

QY 563 GCTGATCAGTCAACACCCGGGGATAATCTGGATTTCGGTTCGGGCTCAAGGTGAAGA 622
DB 541 GCTGATCAGTCAACACCCGGGGATAATCTGGATTTCGGTTCGGGCTCAAGGTGAAGA 600

QY 623 TAATACCTTAAGAGGAGCACTGTAATAATGCCAGAGAGGTGAAGCAACACCAAGTTT 682
DB 601 TAATACCTTAAGAGGAGCACTGTAATAATGCCAGAGAGGTGAAGCAACACCAAGTTT 660

QY 683 AAATGAAGACAGCTGAAACACGCAAGCTGGTTTTATATTAGATATTGACTTAACTA 742
DB 661 AAATGAAGACAGCTGAAACACGCAAGCTGGTTTTATATTAGATATTGACTTAACTA 720

QY 743 TCTCAATAAAGTTTTGACGCTTCCACCAAAAAA 781
DB 721 TCTCAATAAAGTTTTGACGCTTCCACCAAAAAA 759

RESULT 4
AAF68151
ID AAF68151 standard; cdna; 399 BP.
XX
AC AAF68151;
XX
DT 12-APR-2001 (first entry)
XX
DE Human lung tumour protein related nucleotide sequence SEQ ID NO:69.
XX
KW Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
KW lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
KW cytostatic; antisense inhibition; ss.
XX
OS Homo sapiens.
XX
PN WO200100828-A2.
XX
PD 04-JAN-2001.
XX

```
PF 30-JUN-2000; 2000WO-US18061.
XX
PR 30-JUN-1999; 99US-0346492.
PR 15-OCT-1999; 99US-0419356.
PR 17-DEC-1999; 99US-0466867.
PR 30-DEC-1999; 99US-0476300.
PR 06-MAR-2000; 2000US-0519642.
PR 22-MAR-2000; 2000US-0533077.
PR 10-APR-2000; 2000US-0546259.
PR 27-APR-2000; 2000US-0560406.
PR 05-JUN-2000; 2000US-0589184.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
PI Retter MW, Mannion J;
XX
XX WPI; 2001-071488/08.
XX
PT Lung tumor-associated proteins and the nucleic acids that encode them,
PT useful for preventing, diagnosing and treating lung cancer -
XX
PS Claim 4; Page 173; 436pp; English.
XX
XX The present invention describes immunogenic portions of lung tumour-
XX associated proteins (I) and the nucleic acids (NAs) that encode them.
XX (I) have cytostatic activity and can be used in gene therapy, antisense
XX inhibition and in vaccines. The NAs and the lung tumour-associated
XX proteins they encode may be used in the prevention, treatment and
XX diagnosis of diseases associated with their inappropriate expression,
XX especially lung cancers. For example, the NAs may be administered to
XX treat diseases by rectifying mutations or deletions in a patient's genome
XX that affect the activity of the protein by expressing inactive proteins
XX or to supplement the patients own production of (I). Additionally, the
XX NAs may be used to produce the lung-tumour associated protein, according
XX to standard recombinant DNA methodology. Conversely, antisense NA
XX molecules may be administered to down regulate protein expression by
XX binding with the cells own genes and preventing their expression. The NA
XX and complementary sequences may also be used as DNA probes in diagnostic
XX assays to detect and quantitate the presence of similar NA sequences in
XX samples, and hence which patients may be in need of treatment for lung
XX cancer. The (I) may be used as antigens in the production of antibodies
XX and in assays to identify modulators (agonists and antagonists) of the
XX expression and activity of the protein. AAF68083 to AAF68878 and
XX AAF68848 to AAF76878 represent human lung tumour protein related
XX nucleotide and protein sequences which are used in the exemplification
XX of the present invention.
XX
SQ Sequence 399 BP; 150 A; 87 C; 94 G; 67 T; 1 other;
```

```
Query Match 50.0%; Score 390.6; DB 22; Length 399;
Best Local Similarity 98.5%; Pred. No. 5.6e-107;
Matches 393; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 383 GGCATGCGCACACACAAACACAGACAGCCAGTCCCGAGGCGCCAGTAATGG 442
D 1 GACACGCGGACACACAAACACAGACAGCCAGTCCCGAGGCGCCAGTAATGG 60
QY 443 AGACGCCCAAAAGAACACAGCAGCTGAAGTCGGGATCTTACACCTGGGAGCAGAC 502
D 61 AGACGCCCAAAAGAACACAGCAGCTGAAGTCGGGATCTTACACCTGGGATCTTACAC 120
QY 503 AGAAGAAGATCAGATACAGCTGAGATCCAGTCCGCGACATGGAAGTGTATCGCAAGA 562
D 121 AGAAGAAGATCAGATACAGCTGAGATCCAGTCCGCGACATGGAAGTGTATCGCAAGA 180
QY 563 GCTGCATCATGTAACACCGGGGATTAATCTGGATTGGGTTCCGGCGTCAAGTGAAGA 622
D 181 GCTGCATCATGTAACACCGGGGATTAATCTGGATTGGGTTCCGGCGTCAAGTGAAGA 240
QY 623 TAATACCTAAAGAGGAACACTGTAAATGCCAGAAGCAGGTGAAGACCAACCAAGTTT 682
D 241 TAATACCTAAAGAGGAACACTGTAAATGCCAGAAGCAGGTGAAGACCAACCAAGTTT 300
```

```
QY 683 AATGAAGACAAGCTCAAAACACGCAAGCTGTTTATATATAGATATTTTCACTTAACCTA 742
D 301 AATGAAGACAAGCTGAAAACACGCAAGCTGTTTATATATAGATATTTTCACTTAACCTA 360
QY 743 TCTCAATAAAGTTTTCAGCTTTTCACCAAAAAA 781
D 361 TCTCAATAAAGTTTTCAGCTTTTCACCAAAAAA 399
```

```
RESULT 5
AAF68851
ID AAF68851 standard; cDNA; 457 BP.
```

```
XX
AC AAF68851;
XX
DT 12-APR-2001 (first entry)
```

```
XX Human lung tumour protein related nucleotide sequence SEQ ID NO:790.
XX
KW Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
KW lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
KW cytostatic; antisense inhibition; ss.
```

```
XX Homo sapiens.
XX
PN WO200100828-A2.
XX
PD 04-JAN-2001.
```

```
XX 30-JUN-2000; 2000WO-US18061.
XX
PR 30-JUN-1999; 99US-0346492.
PR 15-OCT-1999; 99US-0419356.
PR 17-DEC-1999; 99US-0466867.
PR 30-DEC-1999; 99US-0476300.
PR 06-MAR-2000; 2000US-0519642.
PR 22-MAR-2000; 2000US-0533077.
PR 10-APR-2000; 2000US-0546259.
PR 27-APR-2000; 2000US-0560406.
PR 05-JUN-2000; 2000US-0589184.
XX
XX (CORI-) CORIXA CORP.
```

```
XX Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
PI Retter MW, Mannion J;
XX
XX WPI; 2001-071488/08.
```

```
XX Lung tumor-associated proteins and the nucleic acids that encode them,
XX useful for preventing, diagnosing and treating lung cancer -
XX
XX Claim 4; Page 412; 436pp; English.
```

```
XX The present invention describes immunogenic portions of lung tumour-
XX associated proteins (I) and the nucleic acids (NAs) that encode them.
XX (I) have cytostatic activity and can be used in gene therapy, antisense
XX inhibition and in vaccines. The NAs and the lung tumour-associated
XX proteins they encode may be used in the prevention, treatment and
XX diagnosis of diseases associated with their inappropriate expression,
XX especially lung cancers. For example, the NAs may be administered to
XX treat diseases by rectifying mutations or deletions in a patient's genome
XX that affect the activity of the protein by expressing inactive proteins
XX or to supplement the patients own production of (I). Additionally, the
XX NAs may be used to produce the lung-tumour associated protein, according
XX to standard recombinant DNA methodology. Conversely, antisense NA
XX molecules may be administered to down regulate protein expression by
XX binding with the cells own genes and preventing their expression. The NA
XX and complementary sequences may also be used as DNA probes in diagnostic
XX assays to detect and quantitate the presence of similar NA sequences in
XX samples, and hence which patients may be in need of treatment for lung
XX cancer. The (I) may be used as antigens in the production of antibodies
XX and in assays to identify modulators (agonists and antagonists) of the
```

CC expression and activity of the protein. AAF68083 to AAF68878 and
CC AAB76848 to AAB76878 represent human lung tumour protein related
CC nucleotide and protein sequences which are used in the exemplification
CC of the present invention.

XX Sequence 457 BP; 146 A; 105 C; 121 G; 85 T; 0 other;
SQ
Query Match 47.2%; Score 369; DB 22; Length 457;
Best Local Similarity 98.7%; Pred. No. 1.8e-100;
Matches 372; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 383 GGCATGAGCGACACACACAAACACAGAGACACAGCCAGTCCCGAGGAGCCAGTAATGG 442
DB 81 GACACGGCGACACACAAACACAGAGACACAGCCAGTCCCGAGGAGCCAGTAATGG 140
QY 443 AGAGCCCCAAAAAGAACACAGCAGCTGAAAGTCGGGATCCTACACCTGGGCGAGCAGAC 502
DB 141 AGAGCCCCAAAAAGAACACAGCAGCTGAAAGTCGGGATCCTACACCTGGGCGAGCAGAC 200
QY 503 AGAAGAAGATCAGGATACAGCTGAGATCCAGTGGCGGACATGGAAGGTGATCTGCAAGA 562
DB 201 AGAAGAAGATCAGGATACAGCTGAGATCCAGTGGCGGACATGGAAGGTGATCTGCAAGA 260
QY 563 GCTGCATCAGTCAACACACCGGGGATTAATCTGGATTGGGTTCCCGGCTCAAGGTGAAGA 622
DB 261 GCTGCATCAGTCAACACACCGGGGATTAATCTGGATTGGGTTCCCGGCTCAAGGTGAAGA 320
QY 623 TAATACCTTAAGAGGACACTGTAAATGCCAGAGCAGGTGAAGAGCAACCAACCACTTT 682
DB 321 TAATACCTTAAGAGGACACTGTAAATGCCAGAGCAGGTGAAGAGCAACCAACCAAGTTT 380
QY 683 AAATGAAGCAAGCTGAAACAAACGCAAGCTGTTTTATATTAGATATTGACTTAAACTA 742
DB 381 AAATGAAGCAAGCTGAAACAAACGCAAGCTGTTTTATATTAGATATTGACTTAAACTA 440
QY 743 TCTCAATAAAGTTTTCG 759
DB 441 TCTCAATAAAGTTTTCG 457

RESULT 6
AAL13774
ID AAL13774 standard; cDNA; 618 BP.

XX AAL13774;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 6231.
XX
KW Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.

XX 10-JAN-2001; 2001WO-US00798.
XX
XX 14-JAN-2000; 2000US-0176077.
XX
PR 14-MAR-2000; 2000US-0189167.
XX
PR 24-MAR-2000; 2000US-0192099.
XX
PR 29-MAR-2000; 2000US-0193480.
XX
PR 15-MAY-2000; 2000US-0205230.
XX
PR 09-JUN-2000; 2000US-0211315.
XX
PR 25-JUL-2000; 2000US-0220534.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
XX
XX WPI; 2001-451856/48.

XX New peptide useful as a marker for the diagnosis of breast cancer
XX
XX Claim 1; Page 1118; 3695pp; English.

XX The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.

XX Sequence 618 BP; 169 A; 141 C; 144 G; 119 T; 45 other;
SQ
Query Match 46.3%; Score 361.8; DB 22; Length 618;
Best Local Similarity 93.4%; Pred. No. 3.1e-98;
Matches 369; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 383 GGCATGAGCGACACACAAACACAGAGACACAGCCAGTCCCGAGGAGCCAGTAATGG 442
DB 127 GACACNGCNGACACACAAACACAGAGACACAGCCAGTCCCGAGGAGCCAGTAATGG 186
QY 443 AGAGCCCCAAAAAGAACACAGCAGCTGAAAGTCGGGATCCTACACCTGGGCGAGCAGAC 502
DB 187 AGAGCCCCAAAAAGAACACAGCAGCTGAAAGTCGGGATCCTACACCTGGGCGAGCAGAC 246
QY 503 AGAAGAAGATCAGGATACAGCTGAGATCCAGTGGCGGACATGGAAGGTGATCTGCAAGA 562
DB 247 AGAAGAAGATCAGGATACAGCTGAGATCCAGTGGCGGACATGGAAGGTGATCTGCAAGA 306
QY 563 GCTGCATCAGTCAACACACCGGGGATTAATCTGGATTGGGTTCCCGGCTCAAGGTGAAGA 622
DB 307 GCTGCATCANTCAACACACCGGGGATTAATCTGGATTGGGTTCCCGGCTCAAGGTGAAGA 366
QY 623 TAATACCTTAAGAGGACACTGTAAATGCCAGAGCAGGTGAAGAGCAACCAACCAAGTTT 682
DB 367 TNATACCTTAAGAGGAGCAACACTGTAAATGCCATAGCATGTGAAGAGCAACCAACCAAGTTT 426
QY 683 AAATGAAGCAAGCTGAAACAAACGCAAGCTGTTTTATATTAGATATTGACTTAAACTA 742
DB 427 AAATGAAGCAAGCTGAAACAAACGCAAGCTGTTTTATATTAGATATTGACTTAAACTA 486
QY 743 TCTCAATAAAGTTTTCGAGCTTTCACCAAAAAAAA 777
DB 487 TCTCAATAAAGTTTTCGAGCTTTCACCAAAAAAAA 521

RESULT 7
AAL22641
ID AAL22641 standard; cDNA; 822 BP.

XX AAL22641;
XX
DT 07-DEC-2001 (first entry)
XX
DE Human breast cancer expressed polynucleotide 15098.
XX
KW Human; breast cancer; cell marker; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200151628-A2.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001WO-US00798.
XX
PR 14-JAN-2000; 2000US-0176077.
XX
PR 14-MAR-2000; 2000US-0189167.
XX
PR 24-MAR-2000; 2000US-0192099.

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PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lillie J, Xu Y, Wang Y, Steinmann K;
PI WPI; 2001-451856/48.
XX
XX New peptide useful as a marker for the diagnosis of breast cancer
XX
XX Claim 1; Page 2729-2730; 3695pp; English.
XX
CC The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.
XX
SQ Sequence 822 BP; 255 A; 191 C; 183 G; 181 T; 12 other;
Query Match 45.6%; Score 356.2; DB 22; Length 822;
Best Local Similarity 95.9%; Pred. No. 1.7e-96;
Matches 372; Conservative 0; Mismatches 15; Indels 1; Gaps 1;
Qy 392 GACACACACAAACAGACACAGCCAGTCCCGAGGCCAGTAAATGGAGAGCCCA 451
Dy 112 GACACACACAAACACA-AACCACACAGCCAGTCCCGAGGCCAGTAAATGGAGAGCCCA 170
Qy 452 AAAGAGAGACACAGCAGCTGAAGTCGGGATCCTACACCTGGCGCAGACAGAGAAGA 511
Dy 171 AAAGAATAACACAGCAGCTGAAGTCGGGATCCTACACCTGGCGCAGACAGAGAATAAGA 230
Qy 512 TCAGGATACAGCTGAGATCCAGTCGCGACATGGAGGTGATCTGCAAGAGCTGCATCA 571
Dy 231 TCAGGATACAGCTGAGATCCAGTCGCGACATGGAGGTGATCTGCAAGAGCTGCATCA 290
Qy 572 GTCAAACACCGGGATAAATCTGGATTTGGGTTCCGCGCTCAAGGTGAAGATAATACCTA 631
Dy 291 GTCAAACACCGGGATAAATCTGGATTTGGGTTCCGCGCTCAAGGTGAAGATAATACCTA 350
Qy 632 AAGAGGAACACTGTGTAATGCCAGAGCAGTGAAGAGCAACACCAAGTTTAAATGAAGA 691
Dy 351 AAGAGGAACACTGTGTAATGCCAGAGCAGTGAAGAGCAACCAAGTTTAAATGAAGA 410
Qy 692 CAAGCTGAAACACAGCAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATAA 751
Dy 411 CAAGCTGAAACACAGCAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATAA 470
Qy 752 AGTTTTCAGCTTTCACCAAAAAAAA 779
Dy 471 AGTTTTCAGCTTTCACCAAAAAAAA 498
RESULT 8
AAF68152
ID AAF68152 standard; cDNA; 479 BP.
XX
AC AAF68152;
XX
XX 12-APR-2001 (first entry)
XX
DE Human lung tumour protein related nucleotide sequence SEQ ID NO:70.
XX
KW Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
KW lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
KW cytostatic; antisense inhibition; ss.
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XX Homo sapiens.
XX WO200100828-A2.
XX
XX PD 04-JAN-2001.
XX
XX PF 30-JUN-2000; 2000WO-US18061.
XX
XX PR 30-JUN-1999; 99US-0346492.
XX PR 15-OCT-1999; 99US-0419356.
XX PR 17-DEC-1999; 99US-0466867.
XX PR 30-DEC-1999; 99US-0476300.
XX PR 06-MAR-2000; 2000US-0519642.
XX PR 22-MAR-2000; 2000US-0533077.
XX PR 10-APR-2000; 2000US-0546259.
XX PR 27-APR-2000; 2000US-0560406.
XX PR 05-JUN-2000; 2000US-0589184.
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
PI Retter MW, Mannion J;
XX
XX WPI; 2001-071488/08.
XX
XX Lung tumor-associated proteins and the nucleic acids that encode them,
XX useful for preventing, diagnosing and treating lung cancer
XX
XX Claim 4; Page 174; 436pp; English.
XX
CC The present invention describes immunogenic portions of lung tumour-
CC associated proteins (I) and the nucleic acids (NAs) that encode them.
CC (I) have cytostatic activity and can be used in gene therapy, antisense
CC inhibition and in vaccines. The NAs and the lung tumour-associated
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with their inappropriate expression,
CC especially lung cancers. For example, the NAs may be administered to
CC treat diseases by rectifying mutations or deletions in a patient's genome
CC that affect the activity of the protein by expressing inactive proteins
CC or to supplement the patients own production of (I). Additionally, the
CC NAs may be used to produce the lung-tumour associated protein, according
CC to standard recombinant DNA methodology. Conversely, antisense NA
CC molecules may be administered to down regulate protein expression by
CC binding with the cells own genes and preventing their expression. The NA
CC and complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar NA sequences in
CC samples, and hence which patients may be in need of treatment for lung
CC cancer. The (I) may be used as antigens in the production of antibodies
CC and in assays to identify modulators (agonists and antagonists) of the
CC expression and activity of the protein. AAF68083 to AAF68878 and
CC AAB76848 to AAB76878 represent human lung tumour protein related
CC nucleotide and protein sequences which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 479 BP; 163 A; 107 C; 125 G; 84 T; 0 other;
Query Match 45.3%; Score 354; DB 22; Length 479;
Best Local Similarity 94.7%; Pred. No. 5.9e-96;
Matches 394; Conservative 0; Mismatches 5; Indels 17; Gaps 2;
Qy 383 GGCATGACGCGACACACAAACACACAGACACACAGTCCCGAGGCCAGTAAATGG 442
Dy 64 GACACGGCGGACACACAAACACACAGACACACAGTCCCGAGGCCAGTAAATGG 123
Qy 443 AGAGCCCCAAAAGAAAGAACCCAGCAGCTGAAAGTCGGGATCTTACACCTGGGCGACGAC 502
Dy 124 AGAGCCCCAAAAGAAAGAACCCAGCAGCTGAAAGTCGGGATCTTACACCTGGGCGACGAC 183
Qy 503 AGAAGAACATCAGGATACAGCTGAGATCCCAG-----TGGCGGCACATGG 546
Dy 184 AGAAGAACATCAGGATACAGCTGAGATCCCAGTCTGGGAAGGAGAAATGCGCGACATGG 243
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QY 547 AAGTGATCTGCAAGAGCTGCATCAGTCAACACACCGGGGATAAATCTCGATTGGTTCC 606
DB 244 AAGTGATCTGCAAGAGCTGCATCAGTCAACACACCGGGGATAAATCTCGATTGGTTCC 303
QY 607 GCGTCAAGTCAAGATAATACCTAAAGAGGAACACTGTAAATGCCAGAGCGTCAA 666
DB 304 GCGTCAAGTCAAGATAATACCTAAAGAGGAACACTGTAAATGCCAGAGCGTCAA 363
QY 667 GAGCAACCAAGTTTAAATGAAGACAGCTGAAACACGCAAGCTGGTTTATATTA-G 725
DB 364 GAGCAACCAAGTTTAAATGAAGACAGCTGAAACACGCAAGCTGGTTTATATTAAG 423
QY 726 ATATTTGACTTAACTATCTCAATAAAGTTTTCAGCTTTCACCAAAAAA 781
DB 424 ATATTTGACTTAACTATCTCAATAAAGTTTTCAGCTTTCACCAAAAAA 479
RESULT 9
AAF68852
ID AAF68852 standard; cDNA; 461 BP.
XX
AC AAF68852;
DT
DT 12-APR-2001 (first entry)
XX
DE Human lung tumour protein related nucleotide sequence SEQ ID NO:792.
XX
XX Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
KW lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
KW cytostatic; antisense inhibition; ss.
OS Homo sapiens.
XX
XX WO200100828-A2.
PN
PD 04-JAN-2001.
XX
XX 30-JUN-2000; 2000WO-US18061.
PF
PR 30-JUN-1999; 99US-0346492.
PR 15-OCT-1999; 99US-0419356.
PR 17-DEC-1999; 99US-046867.
PR 30-DEC-1999; 99US-0476300.
PR 06-MAR-2000; 2000US-0519642.
PR 22-MAR-2000; 2000US-053077.
PR 10-APR-2000; 2000US-0546259.
PR 27-APR-2000; 2000US-0560406.
PR 05-JUN-2000; 2000US-0589184.
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Baqur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
PI Retter MW, Mannion J;
XX
XX WPI; 2001-071488/08.
XX
PT Lung tumor-associated proteins and the nucleic acids that encode them,
PT useful for preventing, diagnosing and treating lung cancer -
XX
XX Claim 4; Page 413; 436pp; English.
XX
CC The present invention describes immunogenic portions of lung tumour-
CC associated proteins (I) and the nucleic acids (NAs) that encode them.
CC (I) have cytostatic activity and can be used in gene therapy, antisense
CC inhibition and in vaccines. The NAs and the lung tumour-associated
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with their inappropriate expression,
CC especially lung cancers. For example, the NAs may be administered to
CC treat diseases by rectifying mutations or deletions in a patient's genome
CC that affect the activity of the protein by expressing inactive proteins
CC or to supplement the patients own production of (I). Additionally, the
CC NAs may be used to produce the lung-tumour associated protein, according
CC to standard recombinant DNA methodology. Conversely, antisense NA

CC molecules may be administered to down regulate protein expression by
CC binding with the cells own genes and preventing their expression. The NA
CC and complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar NA sequences in
CC samples, and hence which patients may be in need of treatment for lung
CC cancer. The (I) may be used as antigens in the production of antibodies
CC and in assays to identify modulators (agonists and antagonists) of the
CC expression and activity of the protein. AAF68083 to AAF68878 and
CC AAF68848 to AAF68878 represent human lung tumour protein related
CC nucleotide and protein sequences which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 461 BP; 150 A; 104 C; 123 G; 84 T; 0 other;
Query Match 44.8%; Score 350; DB 22; Length 461;
Best Local Similarity 94.8%; Pred. No. 9.le-95;
Matches 379; Conservative 0; Mismatches 5; Indels 16; Gaps 1;
QY 383 GGCATGAGCGACACACACAAACACAGACCCAGTCCCGAGGAGCCAGTAATGG 442
DB 62 GACACGCGGACACACACAAACACAGAACACACAGCCAGTCCCGAGGAGCCAGTAATGG 121
QY 443 AGAGCCCCAAAGAAAGAACACAGCAGCTGAAAGTCGGGATCTACACCTGGCGACGAC 502
DB 122 AGAGCCCCAAAGAAAGAACACAGCAGCTGAAAGTCGGGATCTACACCTGGCGACGAC 181
QY 503 AGAAGAAGATCAGGATACAGCTGAGATCCAG-----TGCGCGACATGG 546
DB 182 AGAAGAAGATCAGGATACAGCTGAGATCCAGTCTGGAGGAGAAATGCGCGACATGG 241
QY 547 AAGGTGATCTGCAAGAGCTGCATCAGTCAACACACGGGATAAATCTGGATTGGGTCC 606
DB 242 AAGGTGATCTGCAAGAGCTGCATCAGTCAACACACGGGATAAATCTGGATTGGGTCC 301
QY 607 GCGTCAAGTCAAGATAATACCTAAAGAGGAACACTGTAAATGCCAGAGCGTGAA 666
DB 302 GCGTCAAGTCAAGATAATACCTAAAGAGGAACACTGTAAATGCCAGAGCGTGAA 361
QY 667 GAGCAACCAAGTTTAAATGAAGACAGCTGAAACACAGCGAAGCTGGTTTATATTA 726
DB 362 GAGCAACCAAGTTTAAATGAAGACAGCTGAAACACAGCGAAGCTGGTTTATATTA 421
QY 727 TATTTGACTTAACTATCTCAATAAAGTTTTCAGCTTTC 766
DB 422 TATTTGACTTAACTATCTCAATAAAGTTTTCAGCTTTC 461
RESULT 10
AAS38132
ID AAS38132 standard; cDNA; 391 BP.
XX
XX AC AAS38132;
XX
XX DT 17-DEC-2001 (first entry)
XX
XX DE Novel human diagnostic and therapeutic gene #1190.
XX
XX KW Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200166753-A2.
XX
XX PD 13-SEP-2001.
XX
XX PF 09-MAR-2001; 2001WO-US07787.
XX
XX PR 09-MAR-2000; 2000US-0188609.
XX
XX XX (CHIR) CHIRON CORP.
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;


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QY 489 CCTGGCAGCACACAGAAGATCAGGATACAGCTGAGATCCAGTCCGCGACATGGAA 548
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 381 CTGTATCAAGAGAGAGATGATCAGGTGCAGCTGAGATTCAGTGCCTGACCTGGAA 440
QY 549 GGTGATTCGAAGAGCTGCATCAGTCAACACACCGGGGATAAATCTGGATTTGGTTCCGG 608
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 441 GCGATCTCCAGGAGTATGTCAGACAAAGACTGGGATGGATGTGAAGGT-GGTACTGA 499
QY 609 CTTCAAGGTGAAGATAATACCTTAAGAGAGAACACTGTAAATGCCAGAGCAGGTGAAGA 668
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 500 TGTCAAGGGGAAGATCTTACCAAAAGCAGACACTTTAAATGCCAGAGCAGGTGAAGG 559
QY 669 GCAACCAACAAGTTTAAATGAAGACAAAGCTGAAACAAACGCAAGCTGGTTTATATTAGATA 728
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 560 GAAATCACAGGTTTAAAGGAAGATAAGCTGGAACAAACACAAACTCTTTTATATTAGATA 619
QY 729 TTTGAC-TTAACTATCTCAATAAAGTTTTCGAGCTTTCCACCACCAAAAAA 781
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 620 TTTTACTTTAAAAATATCTTAAATAAAGTTTAAAGCTTTTTCACCAAAAAA 673

RESULT 14
AAD14983
ID AAD14983 standard; DNA; 611 BP.
XX
AC AAD14983;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human NOV4 DNA.
XX
KW Human; NOVX; G-antigen; GAGE-like protein; interferon;
KW G-protein coupled receptor; GPCR; hepatocyte nuclear factor;
KW mast cell protease; gene therapy; proliferative disorder; cancer;
KW immune disorder; hepatic disorder; cirrhosis; viral infection;
KW hepatitis; neuroolfactory system-related disorder; neurological disorder;
KW Parkinson's disease; infertility; autoimmune disease; arthritis;
KW multiple sclerosis; allergy; wound healing; cytostatic; neutropenic;
KW immunosuppressive; neuroprotective; vulnerable; vulnery; hepatotropic; ds.
XX
OS Homo sapiens.
XX
FH
FT Key Location/Qualifiers
FT 5'UTR 1..173
FT CDS /*tag= a
FT 174..521
FT /*tag= b
FT /*product= "Human NOV4 protein"
FT 522..611
FT /*tag= c
XX
PN WO200161009-A2.
XX
PD 23-AUG-2001.
XX
PF 15-FEB-2001; 2001WO-US04828.
XX
PR 15-FEB-2000; 2000US-0182723.
PR 15-FEB-2000; 2000US-0182724.
PR 15-FEB-2000; 2000US-0182733.
PR 22-FEB-2000; 2000US-0183896.
PR 23-FEB-2000; 2000US-0184275.
PR 23-FEB-2000; 2000US-0184482.
PR 23-FEB-2000; 2000US-0184497.
PR 24-FEB-2000; 2000US-0184744.
PR 13-APR-2000; 2000US-0197083.
PR 10-AUG-2000; 2000US-0224157.
PR 18-SEP-2000; 2000US-0233405.
PR 27-SEP-2000; 2000US-0236060.
PR 02-JAN-2001; 2001US-0259414.
PR 18-JAN-2001; 2001US-0262454.
PR 14-FEB-2001; 2001US-0783429.
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XX (CURA-) CURAGEN CORP.

PA Malyankar UM, Tchernev VT, Padigaru M, Taupier RJ, Spytek KA;
PI Majumder K, Guo X, Spaderna SK, Boldog FL;

XX WPI: 2001-514775/56.
DR P-PSDB: AAE08583.

XX Isolated novel polypeptides useful for diagnosis of and treating
PT cancer, infertility, autoimmune diseases, arthritis, multiple
PT sclerosis, allergies, wound healing and hepatic disorders -

XX Claim 9; Page 14; 140pp; English.

XX The pres-nt sequence is a human NOV4 DNA. The NOVX protein has homology
CC with one of G-antigen (GAGE)-like protein, interferon, G-protein coupled
CC receptor (GPCR), hepatocyte nuclear factor or mast cell protease. The
CC NOVX is useful for treating or preventing a pathology associated with
CC NOVX. It is also useful for determining the presence or amount of NOVX
CC DNA in a sample, for identifying a potential therapeutic agent and in
CC gene therapy. It is also useful for determining the presence of or
CC predisposition to a disease associated with altered levels of NOVX. It is
CC also useful for the diagnosis and treatment of proliferative disorders,
CC e.g., cancer, immune disorders, hepatic disorders, e.g., cirrhosis, viral
CC infections, e.g., hepatitis, neuroolfactory system-related disorders,
CC neurological disorders, e.g., Parkinson's disease, infertility,
CC autoimmune diseases, arthritis, multiple sclerosis, allergies and wound
XX healing.

XX Sequence 611 BP; 196 A; 127 C; 152 G; 135 T; 1 other;

Query Match 25.8%; Score 201.8; DB 22; Length 611;
Best Local Similarity 78.4%; Pred. No. 3e-50;
Matches 279; Conservative 0; Mismatches 73; Indels 4; Gaps 3;

QY 429 GAGCCCACTATCGAGAGCCCAAAAGAAAGAACAGCAGCTCAAGTCCGGATCCTACA 488
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 255 GAACCCACTGATGAAGAGCCCTAAAGAGAGAAACACCCCACTAAAGTCGGAATCCTACA 314
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 489 CTGGG--CAGCAGACAGAAGAAGATCAGGATACAGCTGAGATCCAGTCCCGGACATGG 546
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 315 CCTGACTCAGAGAGAGAGATGATCAGGGTGCAGCTGAGATTCAGTCCGACCTGG 374
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 547 AAGTGATCTCGAGAGCTGCATCAGTCAACACACCGGGGATAAATCTGGATTTGGTTCC 606
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 375 AAGCGATCTCCAGGAGCTATGTCAGACAAAGACTGGGGATGGATGTGAAGT-GGTACT 433
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 607 GCGTCAAGGTCAAGATAATACCTAAAGAGGAACACTGTAAATGCCAGACAGCTGAA 666
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 434 GATGTCAGGGGAGAGATTCTACCAAAAGCAGAGCACTTTAAATGCCAGACAGGTGAA 493
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 667 GAGCAACCACAAGTTTAAATGAAGACAAGCTGAACACGCAAGCTGTTTATATTAGA 726
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 494 GGAATAATCACAGGTTTAAAGGAAGATAAGCTGAACACACACAAACTGTTTTATATTAGA 553
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 727 TATTGAC-TTAACTATCTCAATAAAGTTTTCAGCTTTCCACCAAAAAA 781
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 554 TATTTACTTTAAAAATATCTTAAATAAAGTTTAAAGCTTTTCTCCAAAAA 609
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15

AAS69484

ID AAS69484 standard; cDNA; 503 BP.

XX AAS69484;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #5288.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Dmanac RT, Liu C, Tang YT;
 XX DR WPI: 2001-639362/73.
 XX DR P-PSDB; ABG05297.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 1; SEQ ID No 5288; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid coding sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SX Sequence 503 BP; 158 A; 98 C; 121 G; 105 T; 21 other;
 Query Match 25.8%; Score 201.2; DB 23; Length 503;
 Best Local Similarity 79.5%; Pred. No. 4.2e-50;
 Matches 275; Conservative 0; Mismatches 6A; Indels 3; Gaps 3;
 QY 426 CAGGAGCCCGAGTAAATGAGAGCCCAAAAGAGAACACAGCAGCTGAAAGTCGGGATCCT 485
 DB 138 CTGGAGCCCGGTGATGAGGAGCCTCAGCAAGAGGAGAACACCACTCAAAAGTCGGGATCCT 197
 QY 486 ACACCTGGGCGACAGACAGAGATCAGGATACAGCTCAGATCCAGTCGCCGACATG 545
 DB 198 GCACCTGGTCAGGAGAGAAAGATCAGGGTTTCAGCTAAGACTCAAGTCCTGACCTG 257
 QY 546 GAAGGTGATCTCGAAGAGCTGCATCAGTCAAAACACCGGGGATAAATCTCGAATTTGGGTTTC 605
 DB 258 GAAGCTGATCTCCAGGAGCTGTCTCAGTCAAAAGACTGGGGTGAAATGTGGAAT-GGTCC 316
 QY 606 CGCGCTCAGAGTGAACATTAATACCTAAAGAGGAGACACTGTAAATGCCAGACAGCTGA 665
 DB 317 TGATGACCGAGGAGAGATTCTGCGAAATATCAGAACAAATTTAAATCCCAAGAGAGTGA 376
 QY 666 AGAGCAACCAAGTTTAAATTAAGACAAGCTGAAACACAGC-AGCTGGTTTATATTA 724
 DB 377 CAGGCAACCAAGTTTAAATTAAGACAAGCTGAAACACCACTGTTTATTTTAA 436

QY 725 GATATTGACTT-AAACTATCTCAATAAAGTTTTCAGCTTTCACC 769
 DB 437 GATATTGACTTAAAAAATATCGAAATAAACTTTTCAGCTTTCCTCC 482
 RESULT 16
 AAC17098
 ID AAC17098 standard; cDNA; 208 BP.
 XX
 AC AAC17098;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 21173.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI: 2000-500381/45.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 1; SEQ ID 21173; 71pp + CD-ROM; English.
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX
 SX Sequence 208 BP; 55 A; 57 C; 70 G; 26 T; 0 other;
 Query Match 25.2%; Score 197; DB 21; Length 208;
 Best Local Similarity 99.5%; Pred. No. 4.7e-49;
 Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 225 TTCTTGTCCTCTCAGCGCCATAACTAGGAGGAAGAGGCGCGAGAGTGGAGGGCTCA 284
 DB 1 TTCTTGTCCTCTCAGCGCCATAACTAGGAGGAAGAGGCGCGAGAGTGGAGGGCTCA 60
 QY 285 GCGCAAGCTGGGGTGTCTGTGGGGGTATCCGAGTCCAGAACACTTGGAAACCCGACAG 344
 DB 61 GCGCAA-CTGGGGTGTCTGTGGGGGTATCCGAGTCCAGAACACTTGGAAACCCGACAG 119
 QY 345 AAGATTCTGACTCCCGACACGGGACAGGAGGAGCGGATGAGCGACACACACAAAC 404
 DB 120 AAGATTCTGACTCCCGACACGGGACAGGAGGAGCGGATGAGCGACACACACAAAC 179

Qy 405 ACAGAACACACAGCCAGTCCCGAGGAGCC 433
Db 180 ACAGAACACACAGCCAGTCCCGAGGAGCC 208

RESULT 17

AAI60530
ID AAI60530 standard; cdna; 532 BP.
AC AAI60530;
XX
XX
XX 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 4519.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.

XX OS Homo sapiens.

XX WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US34263.

XX PR 21-JAN-2000; 2000US-0488725.

XX PR 25-APR-2000; 2000US-0552317.

XX PR 09-JUL-2000; 2000US-0598042.

XX PR 19-JUL-2000; 2000US-0620312.

XX PR 03-AUG-2000; 2000US-0653450.

XX PR 14-SEP-2000; 2000US-0662191.

XX PR 19-OCT-2000; 2000US-0693036.

XX PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao Q, Zhou P, Goodrich R, Drmanac RT;

XX WPI: 2001-442253/47.

XX P-PSDB; AAM41374.

XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

XX Claim 1; SEQ ID NO 4519; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.

XX Note: The sequence data for this patent did not form part of the printed
CC specification.

XX Sequence 532 BP; 154 A; 108 C; 150 G; 120 T; 0 other;

Query Match 25.0%; Score 195.6; DB 22; Length 532;
Best Local Similarity 79.4%; Pred.No. 2e-48; Indels 4; Gaps 4;
Matches 281; Conservative 0; Mismatches 69;
Qy 426 CAGGAGCCAGTAATGGAGAGCCCAAAAGAAAGAACACAGCTGAAAGTCGGATCCT 485
Db 180 CTGGAGCCCGGTGATGAGGAGCCTCAGCAAGAGGAACACCACTGAAAGTCGGATCCT 239
Qy 486 ACACCTGGCCAGCAGACAGAAAGATCAGGATACAGCTGAGATCCAGTCCGACATG 545
Db 240 GCACCTGGTCCAGGAGAGAAAGATCAGGTCAGCTGAGACTCAAGTCCGACCTG 299
Qy 546 GAAAGTGATCTGCAAGAGCTGCATCAGTCAAAACACCGGGGATAAAATCTGGATTTGGTTC 605
Db 300 GAAGCTGATCTCCAGGAGCTGTCTCAGTCAAGAGCTGGGATGAATCGGAGAT-GGTCC 358
Qy 606 CGCGCTCAAGGTGAAGATAATACCTAAAGAGGAACACACTGTGTAAGTCCAGAA-GCAGGTG 664
Db 359 TGATGTCCAGGGGAGAGATTTCTGACAAAGTTCAGAGCAATTTAAATGCCAGAGGAGGTG 418
Qy 665 AAGAGCAACCAACAGTTTAAATGAAGACAGCTGAAACAAACGC-AAGCTGGTTTTATATT 723
Db 419 ACAGGCAACCAACAGTTTAAATGAAGACAGCTGAAACAAACAACTGTTTATCTA 478
Qy 724 AGATATTTGACTT-AAACTATCTCAATAAAGTTTTCAGCTTTCCACCAAAAAA 776
Db 479 AGATATTTGACTTAAATAATATCGAAATAAACTTTTTCAGCTTTCTCCGAAAAA 532

RESULT 18

AAA42613/c

ID AAA42613 standard; cdna; 201 BP.

AC AAA42613;

DT 21-AUG-2000 (first entry)

XX Human secreted expressed sequence tag SEQ ID NO:1353.

XX Human; mouse; xenopus; rat; secreted expressed sequence tag; SEST;
KW expressed sequence tag; EST; probe; chemotactic; proliferative;
KW immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
KW thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
KW antiviral; antidiabetic; neuroprotective; nontropic; antiparkinsonian;
KW cerebrotective; anticonvulsant; antidepressant; gene therapy;
KW vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
KW insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
KW lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KW central nervous system disorder; Alzheimer's disease; stroke;
KW Parkinson's disease; Huntington's disease; coagulation disorder;
KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
KW tumour; infection; depression; psoriasis; ss.

XX OS Homo sapiens.

XX WO200021990-A1.

XX PD 20-APR-2000.

XX PF 15-OCT-1999; 99WO-US24205.

XX PR 15-OCT-1998; 98US-0104435.

XX (GEMY) GENETICS INST INC.

XX Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M;

XX WPI: 2000-317937/27.

XX Isolated polynucleotides, and encoded proteins, comprising secreted
PT expressed sequence tags (sests), useful for treating various disorders

PT such as autoimmune, infectious, and central nervous system disorders -
 XX Claim 1; Page 447; 618pp; English.
 XX AAA41261 to AAA43419 represent specifically claimed secreted expressed
 CC sequence tags (SESTs), isolated from human, mouse, xenopus and rat
 CC tissue sources. The SESTs can have a range of activities depending on
 CC the tissues they were isolated from. The activities include:
 CC chemotactic; proliferative; immunomodulatory; haematopoietic;
 CC chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
 CC cytosstatic; antibacterial; antifungal; antitumor; antidiabetic;
 CC antiasthmatic; vulnerrary; antitumor; osteopathic; neuroprotective;
 CC neurotropic; antiparkinsonian; antipsoriatic; cerebroprotective;
 CC anticonvulsant; and antidepressant. The SESTs can be used for gene
 CC therapy and in vaccines. The SESTs are useful as probes for the
 CC identification and isolation of full-length cDNAs and genomic DNA
 CC molecules which correspond to the SESTs. Proteins encoded by the SESTs
 CC are useful in assays for determining biological activity and raising
 CC antibodies. They may be useful for treatment of autoimmune disorders
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
 CC osteoporosis, osteoarthritis, central nervous system disorders
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
 CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
 CC disease), tumours, bacterial, fungal or viral infections, depression and
 CC psoriasis. AAA43420 to AAA43425 represent linker variants which are given
 CC in the exemplification of the present invention.
 XX SQ Sequence 201 BP; 33 A; 56 C; 42 G; 70 T; 0 other;

Query Match 22.4%; Score 174.8; DB 21; Length 201;
 Best Local Similarity 98.9%; Pred. No. 2.1e-42;
 Matches 176; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 534 GTGCGGCACATGGAGGTGATCTCCAGAGCTGCATCAGTCAACACCGGGGATAAATCT 593
 Db 198 GAGAGCGCATGGAGGTGATCTCCAGAGCTGCATCAGTCAACACCGGGGATAAATCT 139
 Qy 594 GGATTTGGTTCCCGCGTCAAGGTGAAGATAAATACCTAAAGAGGAACACACTGTAATAATGCC 653
 Db 138 GGATTTGGTTCCCGCGTCAAGGTGAAGATAAATACCTAAAGAGGAACACACTGTAATAATGCC 79
 Qy 654 AGAAGCAGGTGAAGAGCAACCAACCAAGTTTAAATGAAGACAGCTGAAACACGCAAGC 711
 Db 78 AGAAGCAGGTGAAGAGCAACCAACCAAGTTTAAATGAAGACAGCTGAAACACGCAAGC 21

RESULT 19
 AAS69486
 ID AAS69486 standard; cDNA: 661 BP.
 XX AAS69486;
 AC AAS69486;
 DT 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #5290.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX Homo sapiens.
 OS
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSEQ -) HYSEQ INC.
 XX

PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG05299.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 1; SEQ ID No 5290; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 661 BP; 212 A; 129 C; 158 G; 162 T; 0 other;
 Query Match 22.0%; Score 171.8; DB 23; Length 661;
 Best Local Similarity 76.9%; Pred. No. 3.2e-41;
 Matches 273; Conservative 0; Mismatches 77; Indels 5; Gaps 5;
 Qy 426 CAGGAGCCCTAGTATGAGAGCCCAAAAGAACAGAACAGCAGCTGAAAGTCGGGATCCT 485
 Db 307 CTGGAGCCCGGTGATGAGGAGCCCTCAGCAAGAGGAACCACTGAAAGTCGGGATCCT 366
 Qy 486 ACACCTGGG-CAGCAGACAGAGAAGATCAGGATACAGCTGAGATCCCGGACAT 544
 Db 367 GCACCTGGGTGAGGAGAGAGAAGATCAGGTCAGCTGAGACTCAAGTCGCTGACCT 426
 Qy 545 GGAAGG-TGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATCTCGATTGGGT 603
 Db 427 GGAAGGCTGATCTCCAGGAGCTGTCTCAGTCAAGAGCTGGGGGTCAATGTGGAATGGTC 486
 Qy 604 TCCGGCGTCAAGGTGAGCATAAATACCTAAAGAGGAACACTGTAAATGCCAGAA-GCAGG 662
 Db 487 CTGATGACCAGGGGAGAGATTCTGCCAATAATCAGAACAAATTTTAAATGCCAAGAGGAGG 546
 Qy 663 TGAAGAGCAACCAAGTTTAAATGAAGACAGCTGAAACACGC-AAGCTGGTTTATA 721
 Db 547 TGACAGGCAACCAAGTTTAAATGAAGACAGCTGAAACACCAACAACTGTTTTTATC 606
 Qy 722 TTAGATATTTGACTT-AAACTATCTCAATAAAGTTTTCAGCTTTCACCAAAAA 775
 Db 607 TAAGATATTTGACTTAAATAATATCGAAATAAATTTTCAGCTTTCCTCAAAAA 661
 RESULT 20
 AAF59637
 ID AAF59637 standard; cDNA: 580 BP.
 XX AAF59637
 AC AAF59637;
 XX
 DT 24-APR-2001 (first entry)
 XX

XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR P-PSDB; ABG27048.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 1; SEQ ID NO 27039; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 750 BP; 225 A; 164 C; 203 G; 158 T; 0 other;
SQ

Query Match 17.8%; Score 139.2; DB 23; Length 750;
Best Local Similarity 77.1%; Pred. No. 2e-31;
Matches 182; Conservative 0; Mismatches 53; Indels 1; Gaps 1;
QY 426 CAGGAGCCAGTAATGCAGAGCCCAAAAGAACAGCAGCTGAAAGTCGGGATCCT 485
DB 208 CAGGAGCCAGTGTGCCAGAGCTCAACNAGAGAACCAACCACTGAAAGTCAGGATCAT 267
QY 486 ACACCTGGGCAGCAGACAGAGAAGATCAGGATACAGCTGAGATCCAGTCGCCGACATG 545
DB 268 ACACCTGGTCAGAGAGAGAAGATGATCAGGTCGAGCTGAGATTCAAGTCGCTAACCTG 327
QY 546 GAAGGTGATCTCAGAGAGCTGCATCAGTCAAAACACCGGGGATAAATCTGGATTGGGTTC 605
DB 328 GAAGCTGATCTCCAGGAGCTGTCTCAGTCAAAAGACTGGGGATGAATGCGGAGAT-AGTCC 386
QY 606 CGCGGTCGAAGGTGAAGATAATACCTAAAGAGGAACACTGTAAATGCCAGAGACAG 661
DB 387 TGATGTCCAGGGAAGATTCTGCCAAAATCAGAGCAATTTAAATATGCCAGAGGAG 442

RESULT 24
AAH83260
ID AAH83260 standard; cDNA; 320 BP.
XX
AC
XX
XX AAH83260;
XX
DT 25-SEP-2001 (first entry)
XX
XX Human ovarian tumour associated polynucleotide sequence SEQ ID NO:884.
DE
XX
KW Human; ovarian tumour; ovarian cancer; diagnosis; gene therapy;
KW immunogenic; vaccine; ss.
XX
XX Homo sapiens.
OS

PN WO200151513-A2.
XX
XX 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01575.
XX
XX 14-JAN-2000; 2000US-0176722.
XX
PA (CORI-) CORIXA CORP.
XX
XX Algate PA;
PI
XX
DR WPI; 2001-425866/45.
XX
XX Novel ovarian tumor proteins, and nucleic acids encoding them, used to
PT treat and diagnose cancers, particularly ovarian cancer -
XX
XX Claim 5; Page 225; 338pp; English.
XX
CC AAH82377 to AAH83878 represent human ovarian tumour-associated
CC polynucleotide sequences which encode ovarian tumour proteins. The
CC ovarian tumour protein and polynucleotide sequences have cytostatic
CC activity, and can be used in gene therapy and vaccine production. The
CC ovarian tumour proteins and polynucleotides can be used to inhibit
CC the development of cancer, particularly ovarian cancer. They can also
CC be used to diagnose the onset and progression of cancer.
XX
SQ Sequence 320 BP; 96 A; 65 C; 85 G; 74 T; 0 other;
Query Match 17.3%; Score 135; DB 22; Length 320;
Best Local Similarity 79.0%; Pred. No. 2.4e-30;
Matches 173; Conservative 0; Mismatches 45; Indels 1; Gaps 1;
QY 523 CTGAGATCCCATGCGGCACATGGAAGCTGATCTGCAAGAGCTGCATCAGTCAAAACCG 582
DB 1 CTGAGATTCAAGTGCCTGACCTGGAGCCGATCTCCAGGAGCTATGTCAGACAAGACTG 60
QY 583 GGGATAAATCTGGATTTGGGTTCCGGCTCAAGGTGAAGATAATACCTAAAGAGAACAC 642
DB 61 GGGATGGATGTGAAGGT-GGTACTGATGTCGAAGGGAAGATTCTACCAAAAAGCAGAC 119
QY 643 TGTAAATGCCAGAGCAGGTGAAGAGCAACCAACCAAGTTTAAATCAAGACAAGCTGAAC 702
DB 120 TTTAAATGCCCAAGCAGGTGAAGGGAATACACAGGTTTAAAGGAAGATAAGCTGAAC 179
QY 703 AACGCAAGCTGTTTATATTAGATATTGACTTAAACT 741
DB 180 AACACAACTGTTTTATATTAGATATTTTACTTTACCT 218

RESULT 25
AAS24637
ID AAS24637 standard; cDNA; 214 BP.
XX
XX
AC AAS24637;
XX
DT 07-NOV-2001 (first entry)
XX
XX Human ovarian PCR-subtracted cDNA library clone #818.
DE
XX
KW Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss;
KW gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
KW primer; probe.
XX
XX Homo sapiens.
OS
XX
XX WO200157207-A2.
PN
XX
PD 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US03733.
PF
XX
XX 04-FEB-2000; 2000US-0180403.
PR

diagnosis; melanoma; antigen; cytolytic T cell clone proliferation;
HLA-typing assay; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 82..436

/*tag= a
/transl_except= (pos:127..129, aa:Arg)
/transl_except= (pos:196..198, aa:Ala)
/transl_except= (pos:199..201, aa:Thr)

W09749417-A1.

31-DEC-1997.

23-JUN-1997; 97WO-US10850.

24-JUN-1996; 96US-0669161.

(LUDW-) LUDWIG INST CANCER RES.

Boon-Falleur T, Debacker O, Van Den Eynde B;

WPI; 1998-076905/07.

P-PSDB; AAW47603.

Isolated nucleic acid encoding GAGE tumour rejection antigen
precursor - processed by HLA-Cw6 molecules into peptides, useful to
diagnose melanomas

Example 13; Fig 4; 60pp; English.

The present sequence encodes a GAGE-6 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various positions, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE cDNAs for the first 112 bases. This region of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants.

Sequence 539 BP; 157 A; 114 C; 157 G; 111 T; 0 other;

Query Match 14.3%; Score 111.6; DB 19; Length 539;
Best Local Similarity 64.2%; Pred. No. 3.3e-23;
Matches 217; Conservative 0; Mismatches 114; Indels 7; Gaps 3;

QY 447 CCCCCAAAGAGAACACGACGCTGAAGTGGGATCCTACACCTGGCGAGCAGACAA 506

DB 202 CCTGAAGAGGGGAACACGACCACTCAAGCTCAGGATCCTGCAGCTGCTCAGGAG---GGA 258

QY 507 GAAGATCAGGATACAGCTGAGATCCAGTGGCGGACATGGAGGTGATCTCAAGAGCTG 566

DB 259 GAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAAGCTGATAGCCAGGAACAG 318

QY 567 CATCAGTCAACACCGGGGATAAATCTGGATTTGGTTCGGCGCTCAAGGTGAAGATAAT 626

DB 319 GGTCAACCCACAGCTGGGTGTGAGTGTGAAGAT--GGTCTGTGGCGAGGAGGTGGACCC 377

QY 627 ACCTAAAGAGGAACACTGTAAATCCAGACGCTGAAGCAACCAACCAAGTTTAAT 686

DB 378 GCCAATCCAGGAGGTGAAGACCCCTGAAGAGGTGAAGCAATCAGAGTGTGTTAAA 437

QY 687 GAAGACAAGCTGAACAAACGCAAGCTGTTTATATTAGATATTG---ACTTAAACTAT 743

DB 438 GAAGACAGCTGAATGATGAGCTGCTCTATGTGAAATTTGTTCAITTAATAATCT 497

QY 744 CTCATAAAGTTTTCAGCTTTCACCAAAAAA 781

DB 498 CCAAATAAGCTTTACAGCTTCTCCAAAAA 535

RESULT 28

AAAX90521

ID AAAX90521 standard; cDNA; 540 BP.

XX AAAX90521;

XX 30-SEP-1999 (first entry)

XX GAGE-4 tumour rejection antigen clone nucleotide sequence.

XX Human leukocyte antigen; HLA-A29; tumour rejection antigen;

XX detection; therapy; pathological condition; cancer; CTL;

XX cytolytic T lymphocyte; GAGE; ss.

XX Homo sapiens.

XX W09937665-A1.

XX 29-JUL-1999.

XX 12-JAN-1999; 99WO-US00775.

XX 23-JAN-1998; 98US-0012818.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Boon-Falleur T, Debacker O, Van Den Eynde B, Van Der Bruggen P;

XX WPI; 1999-469111/39.

XX New isolated peptides which bind to HLA-A29 molecules, which are

XX tumour rejection antigens used for detection and therapy of

XX pathological conditions, e.g. cancer

XX Example 13; Fig 4; 62pp; English.

The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-A29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present invention.

Sequence 540 BP; 159 A; 114 C; 156 G; 111 T; 0 other;

Query Match 14.1%; Score 110; DB 20; Length 540;
Best Local Similarity 63.9%; Pred. No. 9.9e-23;
Matches 216; Conservative 0; Mismatches 115; Indels 7; Gaps 3;

QY 447 CCCCCAAAGAGAACACGACGCTGAAGTGGGATCCTACACCTGGCGACACACAGAA 506

DB 203 CCTGAAGAGGGGAACACGACCACTCAAGCTCAGGATCCTGCAGCTGCTCAGGAG---GGA 259

QY 507 GAAGATCAGGATACAGCTGAGATCCAGTGGCGGACATGGAGGTGATCTCAAGAGCTG 566

DB 260 GAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAGCCTGAAGCTGATAGCCAGACAG 319

QY 567 CATCAGTCAACACCGGGGATAAATCTGGATTTGGTTCGGCGCTCAAGGTGAAGATAAT 626

DB 320 GGTCAACCCACAGCTGGGTGTGAGTGTGAAGAT--GGTCTGTGGCGAGGATGGACCC 378

QY 627 ACCTAAAGAGGAACACTGTAAATGCCAGAGCAGGTGAAGAGCAACCAACCAAGTTTAAT 686

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Db 379 GCCAATCCAGAGGAGGTGAARACGCTGAAGAAGCTGAAGAAGCAATCACAGTGTAAAA 438
Qy 687 GAGACAGCTGAACAACGCAAGCTGTTTATATATAGATATTTG---ACTTAAACTAT 743
Db 439 GAAGCACGTTGAATGATGACGGCTGCTCTATGTTGGAATTTGTTCAATTAATTTCT 498
Qy 744 CTCATAAAGCTTTGCGAGCTTTCCACCAAAAAA 781
Db 499 CCAATAAAGCTTTACAGCCTTCTGCAAAAAA 536

RESULT 29
AA90523
ID AAX90523 standard; cDNA; 540 BP.
XX
AC AAX90523;
XX
DT 30-SEP-1999 (first entry)
XX
DE GAGE-6 tumour rejection antigen clone nucleotide sequence.
XX
KW Human leukocyte antigen; HLA-A29; tumour rejection antigen;
KW detection; therapy; pathological condition; Cancer; CTL;
KW cytolytic T lymphocyte; GAGE; ss.
XX
OS Homo sapiens.
XX
PN WO9937665-A1.
XX
PD 29-JUL-1999.
XX
PF 12-JAN-1999; 99WO-US00775.
XX
PR 23-JAN-1998; 98US-0012818.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, Debacker O, Van Den Eynde B, Van Der Bruggen P;
XX WPI; 1999-469111/39.
XX
DR New isolated peptides which bind to HLA-A29 molecules, which are
XX tumour rejection antigens used for detection and therapy of
XX pathological conditions, e.g. cancer
XX
PS Example 13; Fig 4; 62pp; English.
XX
CC The present invention describes peptides which bind to human leukocyte
CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into
CC tumour rejection antigens. They can be used for detecting cytolytic T
CC lymphocytes (CTLs) in pathological conditions such as cancer and in
CC HLA-typing assays. Complexes of HLA-A29 molecules and the peptides can
CC be used for stimulating CTLs in vivo. The present sequence represents
CC a GAGE tumour rejection antigen clone, from an example from the present
CC invention.
XX
SQ Sequence 540 BP; 159 A; 113 C; 157 G; 111 T; 0 other;
XX
Query Match 14.1%; Score 110; DB 20; Length 540;
Best Local Similarity 63.9%; Pred. NO. 9.9e-23;
Matches 216; Conservative 0; Mismatches 115; Indels 7; Gaps 3;

Qy 447 CCCCCAAAAGAACACAGCAGCTGAAAGTCGGGATCCTACACTGGCCAGCAGACAGAA 506
Db 202 CCTGAAGAGGGGAAACCACTCAACGTCAGGATCCTCGACTGCTCAGGAG---GGA 258
Qy 507 GAAGATCAGGATCAGCTGAGATCCCAAGTCGGGACATGGAAGTGATCTGCAAGAGCTG 566
Db 259 GAGGATGAGGGAGCATCTGCAAGTCAAGGGCCGAAGCCTGAAGCTGATAGCCAGGACAG 318
Qy 567 CATCAGTCAACACCGGGGATAAATCTGGATTTGGGTTCGGCGCTCAAGCTGAAGATAAT 626
Db 319 GGTCAACCCACAGACTGGGTGTGAGTGTGAAGAT-GGTCTGTGAGGAGGAGGTGGACCC 377
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Qy 627 ACCTAAGAGGAACTGTAAATGCCAAGCAGCTGAAGACCAACCAAGTTTAAAT 686
Db 378 GCCAATCCAGAGGAGCTGAACGCTGAAGAAGCTGAAGAAGCAATCACAGTGTAAAA 437
Qy 687 GAGACAGCTGAACAACGCAAGCTGTTTATATATAGATATTTG---ACTTAAACTAT 743
Db 438 GAAGCACGTTGAATGATGACGGCTGCTCTATGTTGGAATTTGTTCAATTAATTTCT 497
Qy 744 CTCATAAAGCTTTGCGAGCTTTCCACCAAAAAA 781
Db 498 CCAATAAAGCTTTACAGCCTTCTGCAAAAAA 535

RESULT 30
AAV18720
ID AAV18720 standard; cDNA; 532 BP.
XX
AC AAV18720;
XX
DT 30-JUL-1998 (first entry)
XX
DE cDNA encoding GAGE-5 tumour rejection antigen precursor.
XX
KW GAGE tumour rejection antigen precursor; TRAP; tumour;
KW diagnosis; melanoma; antigen; cytolytic T cell clone proliferation;
KW HLA-typing assay; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 75..429
FT FT /*tag= a
FT FT /transl_except= (pos:189..191, aa:Ala)
FT FT /transl_except= (pos:192..194, aa:Thr)
XX
PN WO9749417-A1.
XX
PD 31-DEC-1997.
XX
PF 23-JUN-1997; 97WO-US10850.
XX
PR 24-JUN-1996; 96US-0669161.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, Debacker O, Van Den Eynde B;
XX WPI; 1998-076905/07.
XX P-PSDB; AAW47602.
XX
PT Isolated nucleic acid encoding GAGE tumour rejection antigen
PT precursor - processed by HLA-Cw6 molecules into peptides, useful to
XX diagnose melanomas
XX
PS Example 13; Fig 4; 60pp; English.
XX
CC The present sequence encodes a GAGE-5 tumour tumour rejection antigen
XX precursor (TRAP). The protein is expressed in a number of tumours. In
XX contrast the only normal tissue which expresses GAGE TRAP protein is
XX testis. Several GAGE TRAPs have been identified (see AAV18717-21). The
XX major difference between these proteins and GAGE-1 (AAV05540) is the
XX absence of a stretch of 143 bases located at position 379 to 521 of the
XX GAGE-1 TRAP sequence. The rest of the sequences show mismatches at
XX various position, with the exception of GAGE-3 whose 5' end is totally
XX different from the other GAGE cDNAs for the first 112 bases. This
XX region of GAGE-3 cDNA contains a long repeat and a hairpin structure.
XX The antigens can be used to diagnose melanomas, characterised by
XX expression of a TRAP or presentation of a tumour rejection antigen.
XX Antigens shed into blood or urine can be observed and then used to
XX confirm a diagnosis of melanoma using cytolytic T cell clone
XX proliferation methodologies. Other uses for the processed peptides,
XX include HLA-typing assays for, e.g. skin graft or organ transplants.
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XX SQ Sequence 532 BP; 154 A; 110 C; 156 G; 112 T; 0 other;
CC be used for stimulating CTLs in vivo. The present sequence represents
CC a GAGE tumour rejection antigen clone, from an example from the present
CC invention.
XX SQ Sequence 532 BP; 156 A; 111 C; 154 G; 111 T; 0 other;

Query Match 13.9%; Score 108.4; DB 20; Length 532;
Best Local Similarity 63.6%; Pred. No. 3e-22;
Matches 215; Conservative 0; Mismatches 116; Indels 7; Gaps 3;

QY 447 CCCCCAAAGAAAGAACCCAGCAGCTGAAAGTCGGGATCCTACACCTGGGCAGCAGACAGAA 506
DB 195 CCTGAAGAAGGGGAACCAACCACTCAACGTCAGGATCCTGCAGCTGCTCAGGAG---GGA 251

QY 507 GAAGATCAGGATACAGCTGAGATCCCAGTGGCCGACATGGAGGTGATCTCCAAGAGCTG 566
DB 252 GAGGATGAGGGAGCATCTGCAGGTCAAGGCCGGAAGCTGAAGCTGATAGCCAGGAACAG 311

QY 567 CATCAGTCAACACACCGGGGATAATCTGGATTGGGTTCCGGCTCAAGGTGAAGATAAT 626
DB 312 GGTCAACCCACAGACTGGGTGTGAGTGTGAAGAT---GGTCTGATGGCAGGAGATGGACCC 370

QY 627 ACCTAAGAGGAACACTGTAATGCCAAGCAGGTGAAGCAGCAACCAAGTTTAAAT 686
DB 371 GCCAAATCCAGAGGAGGTGAAACGCCCTGAAGAAGGTGAAAGCAATCACAGTGTAAAA 430

QY 687 GAAGACAAGCTGAAACAACGCAAGCTGGTTTATATTAGATATTG---ACTTAACTAT 743
DB 431 GAAGCAGCTTGAATGATGCAGCTCTCTCTATGTTGGAATTTGTCATTAATTTCT 490

QY 744 CTCAATAAAGTTTTCAGCTTTCCACCAAAAAA 781
DB 491 CCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 528

RESULT 31
AA90522
ID AAX90522 standard; cDNA; 532 BP.
AC AAX90522;
XX
XX 30-SEP-1999 (first entry)
XX
DE GAGE-5 tumour rejection antigen clone nucleotide sequence.
KW Human leukocyte antigen; HLA-A29; tumour rejection antigen;
KW detection; therapy; pathological condition; cancer; CTL;
KW cytolytic T lymphocyte; GAGE; ss.
XX
OS Homo sapiens.
XX
PN WO9937665-A1.
XX
PD 29-JUL-1999.
XX
PF 12-JAN-1999; 99WO-US00775.
XX
PR 23-JAN-1998; 98US-0012818.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, Debacker O, Van Den Eynde B, Van Der Bruggen P;
XX WPT; 1999-469111/39.
XX
DR New isolated peptides which bind to HLA-A29 molecules, which are
XX tumour rejection antigens used for detection and therapy of
XX pathological conditions, e.g. cancer
XX
PS Example 13; Fig 4; 62pp; English.
XX
CC The present invention describes peptides which bind to human leukocyte
CC antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into
CC tumour rejection antigens. They can be used for detecting cytolytic T
CC lymphocytes (CTLs) in pathological conditions such as cancer and in
CC HLA-typing assays. Complexes of HLA-29 molecules and the peptides can
```

```
CC be used for stimulating CTLs in vivo. The present sequence represents
CC a GAGE tumour rejection antigen clone, from an example from the present
CC invention.
XX SQ Sequence 532 BP; 156 A; 111 C; 154 G; 111 T; 0 other;

Query Match 13.9%; Score 108.4; DB 20; Length 532;
Best Local Similarity 63.6%; Pred. No. 3e-22;
Matches 215; Conservative 0; Mismatches 116; Indels 7; Gaps 3;

QY 447 CCCCCAAAGAAAGAACCCAGCAGCTGAAAGTCGGGATCCTACACCTGGGCAGCAGACAGAA 506
DB 195 CCTGAAGAAGGGGAACCAACCACTCAACGTCAGGATCCTGCAGCTGCTCAGGAG---GGA 251

QY 507 GAAGATCAGGATACAGCTGAGATCCCAGTGGCCGACATGGAGGTGATCTCCAAGAGCTG 566
DB 252 GAGGATGAGGGAGCATCTGCAGGTCAAGGCCGGAAGCTGAAGCTGATAGCCAGGAACAG 311

QY 567 CATCAGTCAACACACCGGGGATAATCTGGATTGGGTTCCGGCTCAAGGTGAAGATAAT 626
DB 312 GGTCAACCCACAGACTGGGTGTGAGTGTGAAGAT---GGTCTGATGGCAGGAGATGGACCC 370

QY 627 ACCTAAGAGGAACACTGTAATGCCAAGCAGGTGAAGCAGCAACCAAGTTTAAAT 686
DB 371 GCCAAATCCAGAGGAGGTGAAACGCCCTGAAGAAGGTGAAAGCAATCACAGTGTAAAA 430

QY 687 GAAGACAAGCTGAAACAACGCAAGCTGGTTTATATTAGATATTG---ACTTAACTAT 743
DB 431 GAAGCAGCTTGAATGATGCAGCTCTCTCTATGTTGGAATTTGTCATTAATTTCT 490

QY 744 CTCAATAAAGTTTTCAGCTTTCCACCAAAAAA 781
DB 491 CCCAATAAAGCTTTACAGCCTTCTGCAAGAAAAA 528

RESULT 32
AAV18717
ID AAV18717 standard; cDNA; 535 BP.
AC AAV18717;
XX
XX 30-JUL-1998 (first entry)
XX
DE cDNA encoding GAGE-2 tumour rejection antigen precursor.
XX
KW GAGE tumour rejection antigen precursor; TRAP; tumour;
KW diagnosis; melanoma; antigen; cytolytic T cell clone proliferation;
KW HLA-typing assay; ss.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 81..431
XX /*tag= a
XX /transl_except= (pos:192..194, aa:Ala)
XX /transl_except= (pos:195..197, aa:hfr)
XX
XX WO9749417-A1.
XX
XX 31-DEC-1997.
XX
XX 23-JUN-1997; 97WO-US10850.
XX
XX 24-JUN-1996; 96US-0669161.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Boon-Falleur T, Debacker O, Van Den Eynde B;
XX WPI; 1998-076905/07.
XX P-PSDB; AAW47599.
XX
XX Isolated nucleic acid encoding GAGE tumour rejection antigen
XX
```


ID	AAZ97216 standard; cDNA; 1024 BP.
AC	AAZ97216;
DG	18-APR-2000 (first entry)
DE	Human prostate cancer differentially expressed gene #77.
XX	Prostate cancer specific gene; cancer; tumour progression; diagnose;
KW	hyperproliferative cell growth; prostatic disorder; treatment;
KW	metastatic prostate cancer; benign prostate hyperplasia; BPH; ss.
OS	Homo sapiens.
XX	WO9964594-A2.
PX	16-DEC-1999.
PD	10-JUN-1999; 99WO-US13181.
PF	11-JUN-1998; 98US-0088877.
XX	09-JUN-1999; 99US-0088877.
PR	(CHIR) CHIRON CORP.
PA	Astel JH, Carroli E, Endege WO, Ford DM, Monahan JE, Schlegel R;
PI	Steinmann KE, Zhang J;
PX	WIPI; 2000-116541/10.
DR	New isolated prostate cancer specific nucleic acids, used to develop products for the diagnosis and treatment of cancer -
XX	Claim 2; Page 107; 212pp; English.
CC	This sequence represents a prostate cancer specific nucleic acid sequence. The invention relates to a method for diagnosing cancer,
CC	tumour progression, hyperproliferative cell growth or accompanying biological and physical manifestations. The method involves contacting the biological sample with a probe that comprises a sequence capable of hybridising to any of the 339 nucleotide sequences given in the specification (see AAZ97140-297478) and detecting duplex formation. The CC prognosits, and treatment of cancer, tumour progression,
CC	hyperproliferative cell growth, and accompanying physical and biological manifestations. They can be used particularly for prostatic disorders such as metastatic prostate cancer, localised prostate cancer, or benign prostate hyperplasia (BPH).
XX	Sequence 1024 BP; 187 A; 290 C; 232 G; 270 T; 45 other;
SQ	Query Match 13.5%; Score 105.8; DB 21; Length 1024; Best Local Similarity 63.0%; Pred. No. 2.5e-21; Matches 213; Conservative 0; Mismatches 118; Indels 7; Gaps 3;
QY	447 CCCCAAAAAGAACACCAGCTGAAGTGGGATCCTACACCTGGCGGAGCACAGACA 506
DB	450 CCTGAAGAAGGGGAACCAACTAAGTCAGGATCCTGCAGCTGCTCAGGAG--GGA 394
QY	507 GAAGATCAGGTATCAGTGATGCCAGTGCAGCATGGAGGTGATCTGCAAGAGCTG 566
DB	393 GAGATCAGGGAGCATNTGCGAGTCAAGGCCGACACCTGAAGCTCATAGCCAGGNACAG 334
QY	567 CATCAGTCAAACACCGGGATAAATCTGGATTGGTTCCGGCGTCAAGTGAAGATAAT 626
DB	333 GGTCACCCACAGACTGGGTGTGAGTGTGAAGAT-GGTCTGTATGGCAGGATGGACCC 275
QY	627 ACCTTAAGAGGAACACTGTAAATGCCAGACAGCTGAAGCAGCACCAAGTTAAAT 686
DB	274 GCCAAATCCAGAGAGTGAAGACAGCTGAAGAGGTGAAGACCAATCAGATGTTAAAA 215
QY	687 GAAGACAGCTGAACAAACCAAGCTGGTTTTATTATAGATATTG---ACTTAAACTAT 743
Db	214 GAAGGCACGTTGAATGATGCAGCTCTCTATGTGGAAATTTGTCATTAAAAATTC 155
Oy	744 CTCAATAAAGCTTTTGAGCTTTTCAGCTTTTCACCAAAAAAAAAAAAA 781
Db	154 CCATAAAGCTTTTACAGCTTCTGTAAAAA 117
RESULT 40	
AAD14982	
ID	AAD14982 standard; DNA; 1051 BP.
XX	AAAD14982;
AC	AAAD14982;
XX	01-NOV-2001 (first entry)
DT	Human NOV3 DNA.
DE	Human; NOVX; G-antigen; GAGE-like protein; interferon;
XX	G-protein coupled receptor; GPCR; hepatocyte nuclear factor;
KW	mast cell protease; gene therapy; proliferative disorder; cancer;
KW	immune disorder; hepatic disease; cirrhosis; viral infection;
KW	hepatitis; neuroofactory system-related disorder; neurological disorder;
KW	Parkinson's disease; infertility; autoimmune disease; arthritis;
KW	multiple sclerosis; allergy; wound healing; cytostatic; neoplastic;
KW	immunorepressive; neuroprotective; vulnary; hepatotropic; ds.
XX	Homo sapiens.
OS	
XH	Key Location/Qualifiers
FT	5'UTR 1..592
FT	CDS /*tag= a
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FT	929..1051
FT	/*tag= c
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PN	WO200161009-A2.
XX	23-AUG-2001.
PP	15-FEB-2001; 2001WO-US04828.
PR	15-FEB-2000; 2000US-0182723.
PR	15-FEB-2000; 2000US-0182724.
PR	15-FEB-2000; 2000US-0182733.
PR	22-FEB-2000; 2000US-0183896.
PR	23-FEB-2000; 2000US-0184275.
PR	23-FEB-2000; 2000US-0184482.
PR	23-FEB-2000; 2000US-0184497.
PR	24-FEB-2000; 2000US-0184744.
PR	13-APR-2000; 2000US-0197083.
PR	10-AUG-2000; 2000US-0224157.
PR	18-SEP-2000; 2000US-0233405.
PR	27-SEP-2000; 2000US-0236060.
PR	02-JAN-2001; 2001US-0259414.
PR	18-JAN-2001; 2001US-0262454.
PR	14-FEB-2001; 2001US-0783429.
XX	(CURA-) CURAGEN CORP.
XX	Malyankar UM, Tchernev VT, Padigar M, Taupier RJ, Spytek KA;
PI	Malumder K, Guo X, Spaderna SK, Boldog FL;
XX	WPI; 2001-514775/56.
DR	P-PSDS; AAE08582.
XX	Isolated novel polypeptides useful for diagnosis of and treating cancer, infertility, autoimmune diseases, arthritis, multiple sclerosis, allergies, wound healing and hepatic disorders -
PS	Claim 9; Page 11; 140pp; English.

The present sequence is a human NOV3 DNA. The NOVX protein has homology with one of G-antigen (GAG)-like protein, interferon, G-protein coupled receptor (GPCR), hepatocyte nuclear factor or mast cell protease. The NOVX is useful for treating or preventing a pathology associated with NOVX. It is also useful for determining the presence or amount of NOVX DNA in a sample, for identifying a potential therapeutic agent and in gene therapy. It is also useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX. It is also useful for the diagnosis and treatment of proliferative disorders, e.g., cancer, immune disorders, hepatic disorders, e.g., cirrhosis, viral infections, e.g., hepatitis, neurofascory system-related disorders, neurological disorders, e.g., Parkinson's disease, infertility, autoimmune diseases, arthritis, multiple sclerosis, allergies and wound healing.

XX
SQ Sequence 1051 BP; 317 A; 192 C; 257 G; 285 T; 0 other;

Query Match	13.2%	Score 103.2;	DB 22;	Length 1051;
Best Local Similarity	62.8%;	Pred. No. 1.5e-20;		
Matches 230;	Conservative	0;	Mismatches 123;	Indels 13; Gaps 4;
Qy	425	CCAGGAGCCCACTAATGGAGAGCCCAAAAAGAGAAGAACCCAGCAGCTCAAAGTCGGGATCC	484	
Db	679	CCAGGAGCCCACTAGGAAAACACGTCGAAGAGAGAGAACCCACCACTGATATCAAGTGAT	738	
Qy	485	TACACCTGGGCAGCAGAGAAGATCAGGTACAGCTGAGATCCACGTGCCGCGACAT	544	
Db	739	TGCACCTAGTGGGAGAGATTGAAA--ATCAAGCAGTGCCTGCTTTCAAGGGCCTGACAT	795	
Qy	545	GGAAGGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATCTGGATTTGGGTT	604	
Db	796	GGAAGCTTTTCAACAGGAAGCTGGCTCTGCTTGAATAGAGGATGAGCCTGGAGAT-GGTC	854	
Qy	605	CCGGCGTCAAGGTGAAGATATATACCTAAAGAGGAACACTGTAAATGCCAGAACGACGTG	664	
Db	855	CTGATGTCAGGAGGGTATTATGCCACTTTTGATCTCACTAAAGTCTGGAACGACGTG	914	
Qy	665	AAGACAACCACAGTTTAAATGAAGCAA-----GCTGAACACGCAAGCTGGTTTT	718	
Db	915	ATCGCAACCATAGGTTTCAAGCAAGACAAATGAAGACTGAACCAAGAACGTTATTCTT	974	
Qy	719	ATATTAGATATTTCACATTAAACTA---TCTCAATAAAGCTTTTGCAGCTTTTCAACCAAAAA	775	
Db	975	AATCTGGAATTTGACTGATATATCTCTTAATAAAGCTTTAAGTTTCTGCAAGNAA	1034	
Qy	776	AAAAAA	781	
Db	1035	AAAAAA	1040	

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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 4	19	2.4	1607	2	US-07-989-847-1
c 5	19	2.4	1607	3	US-07-721-847A-3
c 6	19	2.4	1607	4	US-08-469-411-1
c 7	19	2.4	1607	4	US-08-925-779-3
c 8	19	2.4	1607	6	5166058-3
c 9	19	2.4	2017	1	US-07-667-276A-3
c 10	19	2.4	2328	4	US-08-811-481-34
c 11	18	2.3	414	1	US-08-377-687-48
c 12	18	2.3	414	1	US-08-771-192-48
c 13	18	2.3	414	4	US-08-971-982-48
c 14	18	2.3	3585	3	US-08-549-846-2
c 15	18	2.3	5137	5	PCT-US96-01314-39
c 16	18	2.3	5138	2	US-08-476-062A-39
c 17	18	2.3	12537	2	US-08-611-280-4
c 18	18	2.3	12537	4	US-09-195-940-4
c 19	17	2.2	708	3	US-08-955-937A-3
c 20	17	2.2	708	4	US-09-300-985-3
c 21	17	2.2	1396	1	US-08-123-161A-11
c 22	17	2.2	1396	1	US-08-483-278-11
c 23	17	2.2	1529	3	US-09-189-760-5
c 24	17	2.2	1529	3	US-09-188-811-5
c 25	17	2.2	1529	4	US-09-514-422-5
c 26	17	2.2	1770	2	US-08-749-289-2
c 27	17	2.2	2080	2	US-08-878-563A-2

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32	17	2.2	2494	3	US-09-514-422-1	Sequence 1, Appli
33	17	2.2	3207	1	US-08-162-081B-35	Sequence 35, Appli
34	17	2.2	3207	2	US-08-780-872-35	Sequence 35, Appli
35	17	2.2	3207	4	US-09-085-957-35	Sequence 35, Appli
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c 43	17	2.2	5143	2	US-08-795-015-7	Sequence 7, Appli
c 44	17	2.2	13104	4	US-08-256-799-4	Sequence 4, Appli
c 45	17	2.2	13104	4	US-08-462-437-4	Sequence 4, Appli
c 46	17	2.2	87350	3	US-08-781-891-79	Sequence 79, Appli
c 47	16	2.0	35	1	US-08-048-975-3	Sequence 3, Appli
c 48	16	2.0	35	1	US-08-438-500-6	Sequence 6, Appli
c 49	16	2.0	35	1	US-08-477-442-6	Sequence 6, Appli
c 50	16	2.0	35	5	PCT-US94-05910-6	Sequence 6, Appli
c 51	16	2.0	311	3	US-08-771-624B-8	Sequence 8, Appli
c 52	16	2.0	311	3	US-09-035-648-6	Sequence 6, Appli
c 53	16	2.0	311	4	US-09-001-951-6	Sequence 6, Appli
c 54	16	2.0	493	1	US-08-203-534-1	Sequence 1, Appli
c 55	16	2.0	506	4	US-09-247-155-69	Sequence 69, Appli
c 56	16	2.0	524	1	US-08-552-142A-8	Sequence 8, Appli
c 57	16	2.0	524	1	US-08-910-973-8	Sequence 8, Appli
c 58	16	2.0	524	5	PCT-US95-05741-8	Sequence 8, Appli
c 59	16	2.0	653	4	US-09-373-750-1	Sequence 1, Appli
c 60	16	2.0	751	4	US-08-936-165A-71	Sequence 71, Appli
c 61	16	2.0	976	1	US-08-125-628-7	Sequence 7, Appli
c 62	16	2.0	976	1	US-08-125-628-8	Sequence 8, Appli
c 63	16	2.0	1113	2	US-08-602-093-2	Sequence 2, Appli
c 64	16	2.0	1140	4	US-09-227-357-53	Sequence 53, Appli
c 65	16	2.0	1142	1	US-08-236-311-9	Sequence 9, Appli
c 66	16	2.0	1142	3	US-08-457-918-9	Sequence 9, Appli
c 67	16	2.0	1195	2	US-08-602-093-1	Sequence 1, Appli
c 68	16	2.0	1208	4	US-09-461-474-11	Sequence 11, Appli
c 69	16	2.0	1251	1	US-08-261-206A-75	Sequence 75, Appli
c 70	16	2.0	1298	3	US-08-948-705-3	Sequence 3, Appli
c 71	16	2.0	1500	3	US-09-052-778-1	Sequence 1, Appli
c 72	16	2.0	1560	1	US-08-552-142A-14	Sequence 14, Appli
c 73	16	2.0	1560	1	US-08-910-973-14	Sequence 14, Appli
c 74	16	2.0	1618	1	US-08-410-540-1	Sequence 1, Appli
c 75	16	2.0	1676	3	US-09-234-332-2	Sequence 2, Appli
c 76	16	2.0	1705	1	US-08-396-452-4	Sequence 4, Appli
c 77	16	2.0	1705	1	US-09-169-119-4	Sequence 4, Appli
c 78	16	2.0	1875	1	US-08-453-956-14	Sequence 14, Appli
c 79	16	2.0	1875	1	US-08-086-631-14	Sequence 14, Appli
c 80	16	2.0	1875	2	US-08-452-930-14	Sequence 14, Appli
c 81	16	2.0	1875	5	PCT-US93-08174-14	Sequence 14, Appli
c 82	16	2.0	1922	4	US-09-382-256-11	Sequence 11, Appli
c 83	16	2.0	1922	4	US-09-395-115-11	Sequence 11, Appli
c 84	16	2.0	1922	4	US-08-436-265-11	Sequence 11, Appli
c 85	16	2.0	2101	3	US-08-765-889C-5	Sequence 5, Appli
c 86	16	2.0	2101	5	PCT-US95-07855-5	Sequence 5, Appli
c 87	16	2.0	2303	2	US-08-480-229C-9	Sequence 9, Appli
c 88	16	2.0	2303	2	US-08-659-235C-9	Sequence 9, Appli
c 89	16	2.0	2308	2	US-08-480-229C-28	Sequence 28, Appli
c 90	16	2.0	2308	2	US-08-659-235C-28	Sequence 28, Appli
c 91	16	2.0	2370	2	US-08-838-219B-19	Sequence 19, Appli
c 92	16	2.0	2370	2	US-08-838-219B-19	Sequence 19, Appli
c 93	16	2.0	2370	3	US-09-233-336A-19	Sequence 19, Appli
c 94	16	2.0	2370	3	US-09-233-336A-19	Sequence 19, Appli
c 95	16	2.0	2403	1	US-09-402-036-19	Sequence 19, Appli
c 96	16	2.0	2403	2	US-08-471-033-30	Sequence 30, Appli
c 97	16	2.0	2403	2	US-08-471-033-30	Sequence 30, Appli
c 98	16	2.0	2403	2	US-08-463-483A-30	Sequence 30, Appli
c 99	16	2.0	2403	2	US-08-471-046A-30	Sequence 30, Appli
c 100	16	2.0	2403	2	US-08-470-566B-30	Sequence 30, Appli
c 101	16	2.0	2403	2	US-08-838-219B-7	Sequence 7, Appli

101	16	2.0	2403	2	US-08-469-334-30	Sequence 30, Appl	c 174	15	1.9	575	1	US-08-507-016-8	Sequence 8, Appl
102	16	2.0	2403	3	US-09-300-529-30	Sequence 30, Appl	c 175	15	1.9	598	4	US-09-247-155-42	Sequence 42, Appl
103	16	2.0	2403	3	US-09-233-336A-7	Sequence 7, Appl	c 176	15	1.9	611	4	US-09-385-982-993	Sequence 393, App
104	16	2.0	2403	3	US-09-233-336A-7	Sequence 7, Appl	c 177	15	1.9	617	4	US-09-385-982-294	Sequence 294, App
105	16	2.0	2403	4	US-09-402-036-7	Sequence 7, Appl	c 178	15	1.9	622	4	US-09-385-982-57	Sequence 57, Appl
106	16	2.0	2502	3	US-09-234-332-1	Sequence 1, Appl	c 179	15	1.9	627	4	US-09-328-111-93	Sequence 93, Appl
107	16	2.0	3225	1	US-08-306-691B-45	Sequence 45, Appl	c 180	15	1.9	635	1	US-08-455-633A-35	Sequence 35, Appl
108	16	2.0	3225	5	PCT-US93-06251-91	Sequence 91, Appl	c 181	15	1.9	635	2	US-08-456-460C-35	Sequence 35, Appl
109	16	2.0	3230	5	PCT-US93-06251-89	Sequence 89, Appl	c 182	15	1.9	635	5	PCT-US94-05354-35	Sequence 327, App
110	16	2.0	3306	1	US-08-261-206A-71	Sequence 71, Appl	c 183	15	1.9	658	4	US-08-896-164-49	Sequence 49, Appl
111	16	2.0	3728	1	US-08-111-939-1	Sequence 1, Appl	c 184	15	1.9	704	4	US-08-896-164-49	Sequence 2, Appl
112	16	2.0	5408	1	US-08-441-139-15	Sequence 15, Appl	c 185	15	1.9	731	3	US-08-451-405A-2	Sequence 173, App
113	16	2.0	5775	1	US-08-306-691B-15	Sequence 15, Appl	c 186	15	1.9	778	3	US-08-961-083-173	Sequence 47, Appl
114	16	2.0	5775	5	PCT-US93-06251-29	Sequence 29, Appl	c 187	15	1.9	790	1	US-08-306-691B-47	Sequence 93, Appl
115	16	2.0	6463	2	US-08-962-284-3	Sequence 3, Appl	c 188	15	1.9	790	5	PCT-US93-06251-93	Sequence 1, Appl
116	16	2.0	11298	1	US-07-869-933-31	Sequence 31, Appl	c 189	15	1.9	792	3	US-08-950-720A-1	Sequence 9, Appl
117	16	2.0	11298	1	US-08-201-879A-2	Sequence 2, Appl	c 190	15	1.9	807	2	US-08-531-927B-9	Sequence 1, Appl
118	16	2.0	11298	4	US-09-103-663-31	Sequence 31, Appl	c 191	15	1.9	812	3	US-08-462-778-1	Sequence 10, Appl
119	16	2.0	17949	4	US-09-087-465-3	Sequence 3, Appl	c 192	15	1.9	826	1	US-08-631-200-10	Sequence 10, Appl
120	16	2.0	31571	1	US-08-223-443B-1	Sequence 1, Appl	c 193	15	1.9	826	1	US-08-829-553-10	Sequence 10, Appl
121	16	2.0	53526	3	US-08-658-136-1	Sequence 2, Appl	c 194	15	1.9	826	2	US-08-922-267A-10	Sequence 10, Appl
122	16	2.0	53577	3	US-08-658-136-1	Sequence 1, Appl	c 195	15	1.9	826	2	US-08-936-707A-10	Sequence 10, Appl
123	16	2.0	80246	4	US-09-078-294-4	Sequence 4, Appl	c 196	15	1.9	826	2	US-08-936-706A-10	Sequence 10, Appl
124	16	2.0	80246	4	US-09-078-294-3	Sequence 3, Appl	c 197	15	1.9	826	3	US-09-248-203-10	Sequence 10, Appl
125	16	2.0	4403765	4	US-09-103-840A-2	Sequence 2, Appl	c 198	15	1.9	826	4	US-09-406-071-10	Sequence 10, Appl
126	16	2.0	4411529	4	US-09-103-840A-1	Sequence 1, Appl	c 199	15	1.9	854	4	US-09-064-693A-24	Sequence 24, Appl
127	15	1.9	15	3	US-08-832-021-52	Sequence 52, Appl	c 200	15	1.9	856	1	US-08-374-983A-12	Sequence 12, Appl
128	15	1.9	24	2	US-08-704-682-1	Sequence 1, Appl	c 201	15	1.9	857	4	US-08-998-416-555	Sequence 555, App
129	15	1.9	30	3	US-08-836-329-9	Sequence 9, Appl	c 202	15	1.9	866	4	US-09-227-357-97	Sequence 97, Appl
130	15	1.9	38	1	US-08-222-177A-68	Sequence 68, Appl	c 203	15	1.9	911	4	US-09-364-230-25	Sequence 25, Appl
131	15	1.9	40	4	US-09-306-290-2	Sequence 2, Appl	c 204	15	1.9	912	3	US-08-688-988-3	Sequence 3, Appl
132	15	1.9	40	4	US-09-306-290-5	Sequence 5, Appl	c 205	15	1.9	948	1	US-09-247-155-50	Sequence 50, Appl
133	15	1.9	40	4	US-09-306-290-9	Sequence 9, Appl	c 206	15	1.9	960	4	US-07-639-330E-1	Sequence 1, Appl
134	15	1.9	40	4	US-08-150-156A-37	Sequence 37, Appl	c 207	15	1.9	1020	4	US-09-247-155-143	Sequence 4, Appl
135	15	1.9	42	4	US-08-306-290-13	Sequence 13, Appl	c 208	15	1.9	1029	4	US-09-077-675A-4	Sequence 127, App
136	15	1.9	44	1	US-08-222-177A-249	Sequence 249, App	c 209	15	1.9	1048	4	US-09-227-357-127	Sequence 2, Appl
137	15	1.9	51	1	US-08-222-177A-325	Sequence 325, App	c 210	15	1.9	1095	1	US-08-389-668A-3	Sequence 3, Appl
138	15	1.9	51	2	US-08-704-682-2	Sequence 2, Appl	c 211	15	1.9	1106	1	US-08-732-506-3	Sequence 3, Appl
139	15	1.9	72	1	US-08-222-177A-131	Sequence 131, App	c 212	15	1.9	1106	5	PCT-US95-05768-3	Sequence 5, Appl
140	15	1.9	72	1	US-08-222-177A-427	Sequence 427, App	c 213	15	1.9	1106	4	US-08-664-962B-5	Sequence 5, Appl
141	15	1.9	75	2	US-08-776-944-13	Sequence 13, Appl	c 214	15	1.9	1109	4	US-08-311-743-5	Sequence 5, Appl
142	15	1.9	92	1	US-08-222-177A-430	Sequence 430, App	c 215	15	1.9	1115	1	US-08-784-651-9	Sequence 9, Appl
143	15	1.9	98	1	US-08-399-412A-77	Sequence 77, Appl	c 216	15	1.9	1117	2	US-08-960-022-1	Sequence 1, Appl
144	15	1.9	130	6	5198345-15	Patent No. 5198345	c 217	15	1.9	1188	2	US-08-557-128-10	Sequence 10, Appl
145	15	1.9	194	1	US-08-222-177A-15	Sequence 15, Appl	c 218	15	1.9	1191	1	US-08-687-379-13	Sequence 13, Appl
146	15	1.9	216	4	US-09-439-313-425	Sequence 425, App	c 219	15	1.9	1191	1	US-08-687-379-15	Sequence 15, Appl
147	15	1.9	228	3	US-08-688-988-25	Sequence 25, App	c 220	15	1.9	1212	3	US-09-058-489-43	Sequence 43, Appl
148	15	1.9	294	1	US-08-446-660-18	Sequence 18, Appl	c 221	15	1.9	1220	1	US-08-374-983A-14	Sequence 14, Appl
149	15	1.9	294	4	US-08-974-302-18	Sequence 18, Appl	c 222	15	1.9	1234	1	US-08-798-000-1	Sequence 1, Appl
150	15	1.9	300	1	US-08-333-358-5	Sequence 5, Appl	c 223	15	1.9	1260	1	US-08-599-252-79	Sequence 79, Appl
151	15	1.9	300	1	US-08-463-694-5	Sequence 5, Appl	c 224	15	1.9	1260	5	PCT-US96-06352-79	Sequence 52, Appl
152	15	1.9	300	1	US-08-694-501-5	Sequence 5, Appl	c 225	15	1.9	1260	5	PCT-US96-06583-79	Sequence 79, Appl
153	15	1.9	301	5	PCT-US94-05150-20	Sequence 20, Appl	c 226	15	1.9	1260	5	PCT-US96-06583-79	Sequence 79, Appl
154	15	1.9	332	2	US-08-469-412A-8	Sequence 8, Appl	c 227	15	1.9	1268	4	US-09-303-064-23	Sequence 23, Appl
155	15	1.9	332	3	US-09-021-715-8	Sequence 7, Appl	c 228	15	1.9	1268	4	US-09-086-503-23	Sequence 23, Appl
156	15	1.9	342	3	US-09-014-877A-7	Sequence 7, Appl	c 229	15	1.9	1289	4	US-09-247-155-138	Sequence 138, App
157	15	1.9	390	4	US-09-385-982-232	Sequence 232, App	c 230	15	1.9	1315	4	US-08-992-035A-2	Sequence 2, Appl
158	15	1.9	446	1	US-08-104-072B-1	Sequence 1, Appl	c 231	15	1.9	1333	4	US-09-247-155-77	Sequence 77, Appl
159	15	1.9	474	2	US-08-619-542B-45	Sequence 45, Appl	c 232	15	1.9	1372	6	5189147-2	Patent No. 5189147
160	15	1.9	492	2	US-08-892-880-12	Sequence 12, Appl	c 233	15	1.9	1374	1	US-08-278-630A-9	Sequence 9, Appl
161	15	1.9	513	4	US-09-268-364-7	Sequence 7, Appl	c 234	15	1.9	1380	2	US-08-467-559B-1	Sequence 1, Appl
162	15	1.9	533	1	US-08-104-073-1	Sequence 1, Appl	c 235	15	1.9	1387	3	US-08-868-594-1	Sequence 1, Appl
163	15	1.9	534	1	US-08-599-252-101	Sequence 101, App	c 236	15	1.9	1387	4	US-09-434-323-1	Sequence 4, Appl
164	15	1.9	534	5	PCT-US96-06352-101	Sequence 101, App	c 237	15	1.9	1430	2	US-08-204-288-4	Sequence 8, Appl
165	15	1.9	534	5	PCT-US96-06583-101	Sequence 101, App	c 238	15	1.9	1512	3	US-08-909-965C-8	Sequence 141, App
166	15	1.9	535	4	US-09-385-982-385	Sequence 385, App	c 239	15	1.9	1519	3	US-08-592-900-1	Sequence 1, Appl
167	15	1.9	536	4	US-09-385-982-347	Sequence 347, App	c 240	15	1.9	1566	4	US-09-276-357-141	Sequence 75, App
168	15	1.9	558	4	US-08-976-259-53	Sequence 53, Appl	c 241	15	1.9	1567	4	US-09-276-351-75	Sequence 1, Appl
169	15	1.9	560	2	US-08-365-486A-7	Sequence 7, Appl	c 242	15	1.9	1597	2	US-08-724-974A-1	Sequence 1, Appl
170	15	1.9	560	4	US-08-880-342-7	Sequence 7, Appl	c 243	15	1.9	1619	3	US-09-163-162-1	Sequence 1, Appl
171	15	1.9	566	4	US-09-385-982-468	Sequence 468, App	c 244	15	1.9	1619	4	US-09-286-407-1	Sequence 1, Appl
172	15	1.9	569	4	US-09-227-357-89	Sequence 89, App	c 245	15	1.9	1619	4	US-09-286-407-1	Sequence 1, Appl
173	15	1.9	574	4	US-09-385-982-463	Sequence 463, App	c 246	15	1.9	1619	4	US-09-286-407-1	Sequence 1, Appl

c 247	15	1.9	1619	4	US-09-496-694B-97	Sequence 97, Appl	320	15	1.9	2584	5	PCT-US93-08322-1	Sequence 1, Appli
248	15	1.9	1632	2	US-08-892-715-1	Sequence 1, Appli	321	15	1.9	2610	2	US-08-989-386-2	Sequence 2, Appli
249	15	1.9	1632	2	US-09-145-947-1	Sequence 1, Appli	322	15	1.9	2628	1	US-08-143-219-1	Sequence 1, Appli
250	15	1.9	1632	4	US-09-265-642-1	Sequence 1, Appli	323	15	1.9	2647	5	PCT-US93-06251-77	Sequence 77, Appl
251	15	1.9	1633	1	US-08-197-792-42	Sequence 42, Appl	324	15	1.9	2658	2	US-08-592-383-3	Sequence 3, Appli
252	15	1.9	1633	1	US-08-459-850-42	Sequence 42, Appl	325	15	1.9	2658	2	US-08-826-426-14	Sequence 14, Appl
253	15	1.9	1633	1	US-08-459-214-42	Sequence 42, Appl	326	15	1.9	2659	3	US-08-749-522-1	Sequence 1, Appli
254	15	1.9	1644	2	US-08-458-555-1	Sequence 1, Appli	327	15	1.9	2684	2	US-08-984-171-2	Sequence 2, Appli
255	15	1.9	1648	4	US-09-303-064-26	Sequence 26, Appl	328	15	1.9	2688	2	US-08-909-965C-1	Sequence 1, Appli
256	15	1.9	1648	4	US-09-086-503-26	Sequence 26, Appl	329	15	1.9	2738	2	US-08-795-868-17	Sequence 17, Appl
257	15	1.9	1679	4	US-09-271-437-3	Sequence 3, Appli	330	15	1.9	2738	4	US-09-303-069-17	Sequence 17, Appl
258	15	1.9	1708	3	US-09-108-020-5	Sequence 5, Appli	331	15	1.9	2770	4	US-08-426-509A-5	Sequence 5, Appli
259	15	1.9	1715	1	US-07-847-743B-24	Sequence 24, Appl	332	15	1.9	2770	5	PCT-US95-05008-5	Sequence 31, Appli
260	15	1.9	1715	1	US-08-456-201-24	Sequence 24, Appl	c 333	15	1.9	2811	1	US-08-040-548-31	Sequence 31, Appl
261	15	1.9	1715	2	US-08-456-241-24	Sequence 24, Appl	c 334	15	1.9	2811	1	US-08-466-344-31	Sequence 31, Appl
262	15	1.9	1715	5	PCT-US92-04295A-24	Sequence 24, Appl	c 335	15	1.9	2817	6	5206152-6	Patent No. 5206152
c 263	15	1.9	1724	4	US-09-153-804-8	Sequence 8, Appli	336	15	1.9	2928	2	US-08-095-728B-3	Sequence 3, Appli
264	15	1.9	1733	3	US-09-147-522-1	Sequence 1, Appli	337	15	1.9	2928	5	PCT-US92-02320A-3	Sequence 3, Appli
265	15	1.9	1776	2	US-08-531-927B-1	Sequence 1, Appli	338	15	1.9	2940	2	US-08-592-383-1	Sequence 1, Appli
266	15	1.9	1776	4	US-09-041-886-12	Sequence 12, Appl	339	15	1.9	2940	6	5171671-1	Patent No. 5171671
267	15	1.9	1791	1	US-08-245-294-7	Sequence 7, Appli	c 340	15	1.9	2946	3	US-08-968-563-6	Sequence 6, Appli
268	15	1.9	1791	1	US-08-474-499-7	Sequence 7, Appli	c 341	15	1.9	2946	3	US-08-969-683A-6	Sequence 6, Appli
269	15	1.9	1791	1	US-08-307-279A-7	Sequence 7, Appli	c 342	15	1.9	2946	4	US-09-297-928-2	Sequence 2, Appli
270	15	1.9	1791	5	PCT-US95-06211-7	Sequence 7, Appli	c 343	15	1.9	2977	2	US-08-820-170A-36	Sequence 36, Appl
271	15	1.9	1840	2	US-08-484-993B-15	Sequence 15, Appl	c 344	15	1.9	2977	3	US-09-055-699-36	Sequence 36, Appl
272	15	1.9	1840	2	US-08-484-158B-15	Sequence 15, Appl	c 345	15	1.9	2977	4	US-09-273-565-36	Sequence 36, Appl
273	15	1.9	1840	2	US-08-484-596A-15	Sequence 15, Appl	c 346	15	1.9	2977	4	US-09-565-538-36	Sequence 36, Appl
274	15	1.9	1840	2	US-08-480-150A-15	Sequence 15, Appl	c 347	15	1.9	3046	1	US-08-726-725-1	Sequence 1, Appli
275	15	1.9	1840	3	US-08-458-731-15	Sequence 15, Appl	c 348	15	1.9	3113	1	US-08-146-422-20	Sequence 20, Appl
276	15	1.9	1840	3	US-08-149-223A-15	Sequence 15, Appl	c 349	15	1.9	3113	1	US-08-626-554-2	Sequence 2, Appli
277	15	1.9	1847	3	US-08-930-894-3	Sequence 3, Appli	c 350	15	1.9	3132	3	US-09-286-904-45	Sequence 45, Appl
278	15	1.9	1854	3	US-08-923-454A-13	Sequence 13, Appl	c 351	15	1.9	3134	2	US-08-533-669A-1	Sequence 1, Appli
c 279	15	1.9	1857	2	US-08-537-715-3	Sequence 3, Appli	c 352	15	1.9	3219	2	US-08-687-289A-3	Sequence 3, Appli
280	15	1.9	1857	5	US-09-377-557-9	Sequence 9, Appli	c 353	15	1.9	3219	2	US-08-687-289A-4	Sequence 4, Appli
c 281	15	1.9	1857	5	PCT-US94-04173-3	Sequence 3, Appli	354	15	1.9	3256	2	US-08-968-751-3	Sequence 3, Appli
282	15	1.9	1863	3	US-09-199-229-1	Sequence 1, Appli	355	15	1.9	3358	3	US-08-957-063-4	Sequence 4, Appli
283	15	1.9	1863	3	US-09-443-087-1	Sequence 1, Appli	356	15	1.9	3358	4	US-09-487-685-4	Sequence 4, Appli
284	15	1.9	1863	4	US-09-687-298-1	Sequence 1, Appli	c 357	15	1.9	3366	1	US-08-469-802B-1	Sequence 1, Appli
c 285	15	1.9	1864	1	US-08-454-720A-38	Sequence 38, Appl	c 358	15	1.9	3366	2	US-08-267-803B-1	Sequence 1, Appli
286	15	1.9	1894	2	US-08-935-450-7	Sequence 7, Appli	c 359	15	1.9	3376	1	US-08-320-559-29	Sequence 29, Appl
287	15	1.9	1965	1	US-08-258-420-9	Sequence 9, Appli	c 360	15	1.9	3376	5	PCT-US94-04496-29	Sequence 29, Appl
288	15	1.9	1975	1	US-08-484-105-11	Sequence 11, Appl	c 361	15	1.9	3376	5	PCT-US94-04496-29	Sequence 1, Appli
289	15	1.9	1975	1	US-08-484-106-11	Sequence 11, Appl	c 362	15	1.9	3384	2	US-08-687-289A-1	Sequence 1, Appli
290	15	1.9	2001	3	US-08-850-961-13	Sequence 13, Appl	c 363	15	1.9	3387	1	US-08-468-557-1	Sequence 1, Appli
291	15	1.9	2001	4	US-09-479-776-13	Sequence 13, Appl	364	15	1.9	3393	1	US-08-295-502-1	Sequence 1, Appli
292	15	1.9	2124	4	US-09-198-122-1	Sequence 1, Appli	365	15	1.9	3393	5	PCT-US95-10691-1	Sequence 1, Appli
293	15	1.9	2152	4	US-08-188-582-17	Sequence 17, Appl	366	15	1.9	3396	2	US-08-974-565C-6	Sequence 6, Appli
294	15	1.9	2152	1	US-08-646-715-17	Sequence 17, Appl	367	15	1.9	3396	3	US-09-255-748-6	Sequence 6, Appli
295	15	1.9	2162	2	US-08-870-518-5	Sequence 5, Appli	368	15	1.9	3402	1	US-08-480-917-1	Sequence 1, Appli
c 296	15	1.9	2186	3	US-08-959-382-1	Sequence 1, Appli	c 369	15	1.9	3402	1	US-08-480-917-1	Sequence 1, Appli
297	15	1.9	2201	2	US-08-974-565C-2	Sequence 2, Appli	370	15	1.9	3402	4	US-09-138-736-1	Sequence 1, Appli
298	15	1.9	2201	3	US-09-255-748-2	Sequence 2, Appli	c 371	15	1.9	3402	4	US-09-138-736-1	Sequence 1, Appli
299	15	1.9	2214	4	US-08-943-731-57	Sequence 57, Appl	372	15	1.9	3407	1	US-08-253-155A-7	Sequence 7, Appli
300	15	1.9	2226	2	US-08-031-538-1	Sequence 1, Appli	373	15	1.9	3461	2	US-08-389-564B-1	Sequence 1, Appli
301	15	1.9	2229	1	US-08-624-663A-1	Sequence 1, Appli	374	15	1.9	3461	3	US-08-466-047B-1	Sequence 1, Appli
302	15	1.9	2313	2	US-08-892-880-1	Sequence 1, Appli	c 375	15	1.9	3474	4	US-09-527-236A-1	Sequence 1, Appli
303	15	1.9	2385	1	US-08-393-333-1	Sequence 1, Appli	376	15	1.9	3487	4	US-09-303-069-24	Sequence 24, Appl
304	15	1.9	2387	3	US-08-891-845-11	Sequence 11, Appl	377	15	1.9	3490	2	US-08-841-483-3	Sequence 3, Appli
305	15	1.9	2418	3	US-09-011-074-3	Sequence 3, Appli	378	15	1.9	3490	4	US-09-382-911-3	Sequence 3, Appli
c 306	15	1.9	2430	2	US-08-820-170A-35	Sequence 35, Appl	c 379	15	1.9	3600	3	US-08-894-731-1	Sequence 9, Appli
307	15	1.9	2430	3	US-09-055-699-35	Sequence 35, Appl	c 380	15	1.9	3714	4	US-09-087-465-9	Sequence 9, Appli
c 308	15	1.9	2430	4	US-09-273-565-35	Sequence 35, Appl	c 381	15	1.9	3804	2	US-08-483-488-5	Sequence 5, Appli
c 309	15	1.9	2430	4	US-09-565-538-35	Sequence 35, Appl	382	15	1.9	4094	2	US-08-841-483-5	Sequence 5, Appli
310	15	1.9	2467	1	US-08-148-5810-1	Sequence 1, Appli	383	15	1.9	4094	4	US-09-382-911-5	Sequence 29, Appl
311	15	1.9	2498	1	US-07-943-843-3	Sequence 3, Appli	384	15	1.9	4146	4	US-08-952-089A-29	Sequence 29, Appl
312	15	1.9	2498	1	US-08-347-003-3	Sequence 3, Appli	c 385	15	1.9	4300	1	US-08-041-538-1	Sequence 1, Appli
313	15	1.9	2520	4	US-08-931-608A-2	Sequence 2, Appli	c 386	15	1.9	4300	1	US-08-463-642-1	Sequence 1, Appli
314	15	1.9	2570	2	US-08-448-603A-31	Sequence 31, Appl	c 387	15	1.9	4300	1	US-08-455-602-1	Sequence 1, Appli
315	15	1.9	2570	3	US-09-134-075-31	Sequence 31, Appl	c 388	15	1.9	4300	2	US-08-465-157-1	Sequence 1, Appli
316	15	1.9	2584	1	US-08-121-714-1	Sequence 1, Appli	c 389	15	1.9	4300	5	PCT-US91-09422-1	Sequence 1, Appli
317	15	1.9	2584	1	US-08-322-742-13	Sequence 13, Appl	c 390	15	1.9	4360	1	US-08-470-350B-1	Sequence 1, Appli
318	15	1.9	2584	1	US-08-477-108A-1	Sequence 1, Appli	c 391	15	1.9	4405	1	US-07-885-972A-3	Sequence 3, Appli
319	15	1.9	2584	2	US-08-477-112-1	Sequence 1, Appli	392	15	1.9	4405	2	US-08-745-880-3	Sequence 3, Appli

393	15	1.9	4405	2	US-08-480-382-3	Sequence 3, Appli	c 466	15	1.9	17410	2	US-08-449-700-3	Sequence 3, Appli
394	15	1.9	4437	1	US-08-559-303B-72	Sequence 72, Appl	c 467	15	1.9	17410	2	US-08-449-699A-3	Sequence 3, Appli
395	15	1.9	4437	1	US-09-175-828-72	Sequence 72, Appl	c 468	15	1.9	17415	5	US-08-486-343A-1	Sequence 1, Appli
396	15	1.9	4543	2	US-08-519-547A-5	Sequence 5, Appli	c 469	15	1.9	17415	5	PCT-US95-07349-1	Sequence 1, Appli
397	15	1.9	4698	1	US-07-807-043B-5	Sequence 5, Appli	c 470	15	1.9	18609	4	US-08-943-731-1	Sequence 7, Appli
398	15	1.9	4698	1	US-08-299-849B-5	Sequence 5, Appli	c 471	15	1.9	28720	4	US-09-341-587-7	Sequence 207, App
399	15	1.9	4698	2	US-08-142-368A-5	Sequence 5, Appli	c 472	15	1.9	29604	3	US-08-781-891-207	Sequence 7, Appli
400	15	1.9	4698	3	US-08-967-727-5	Sequence 5, Appli	c 473	15	1.9	35060	3	US-08-814-095-7	Sequence 19, Appl
401	15	1.9	4698	4	US-08-037-230B-5	Sequence 5, Appli	c 474	15	1.9	35100	5	PCT-US93-06251-19	Sequence 19, Appl
402	15	1.9	4718	3	US-08-936-135-9	Sequence 8, Appli	c 475	15	1.9	35100	5	US-08-742-185-101	Sequence 101, App
403	15	1.9	4724	4	US-09-194-285-8	Sequence 11, Appl	c 476	15	1.9	48974	4	US-08-920-422-17	Sequence 17, Appl
404	15	1.9	4733	3	US-08-936-135-11	Sequence 1, Appli	c 477	15	1.9	48974	4	US-08-920-422-17	Sequence 3, Appli
405	15	1.9	4749	1	US-08-452-259-1	Sequence 1, Appli	c 478	15	1.9	59065	4	US-09-813-817-3	Sequence 1, Appli
406	15	1.9	4749	5	PCT-US96-07336-1	Sequence 13, Appl	c 479	15	1.9	72928	3	US-09-009-913-1	Sequence 1, Appli
407	15	1.9	4769	3	US-08-936-135-13	Sequence 15, Appl	c 480	15	1.9	80161	3	US-09-036-987A-1	Sequence 1, Appli
408	15	1.9	4784	3	US-08-936-135-15	Sequence 1, Appli	c 481	15	1.9	80161	3	US-09-370-700-1	Sequence 3, Appli
409	15	1.9	4821	3	US-08-913-374-1	Sequence 4, Appli	c 482	15	1.9	80246	4	US-09-078-294-4	Sequence 4, Appli
410	15	1.9	5110	2	US-08-404-531B-4	Sequence 5, Appli	c 483	15	1.9	80246	4	US-09-078-294-4	Sequence 3, Appli
411	15	1.9	5110	2	US-08-404-531B-5	Sequence 4, Appli	c 484	15	1.9	80246	4	US-09-078-294-4	Sequence 3, Appli
412	15	1.9	5110	3	US-08-476-900A-5	Sequence 4, Appli	c 485	15	1.9	84495	4	US-09-797-906-3	Sequence 16, Appl
413	15	1.9	5110	3	US-08-476-900A-5	Sequence 4, Appli	c 486	15	1.9	84495	4	US-09-797-906-3	Sequence 16, Appl
414	15	1.9	5110	3	US-08-488-546A-4	Sequence 5, Appli	c 487	15	1.9	152331	3	US-09-128-155-16	Sequence 17, Appl
415	15	1.9	5110	3	US-08-488-546A-5	Sequence 5, Appli	c 488	15	1.9	152331	3	US-09-128-155-16	Sequence 17, Appl
416	15	1.9	5236	5	PCT-US91-09422-16	Sequence 16, Appl	c 489	15	1.9	246240	2	US-08-724-394A-20	Sequence 20, Appl
417	15	1.9	5261	1	US-08-045-806-3	Sequence 3, Appli	c 490	15	1.9	246240	2	US-08-724-394A-21	Sequence 21, Appl
418	15	1.9	5261	1	US-08-366-051B-3	Sequence 3, Appli	c 491	15	1.9	246240	2	US-08-724-394A-22	Sequence 22, Appl
419	15	1.9	5526	3	US-08-751-359-21	Sequence 21, Appl	c 492	15	1.9	246240	2	US-08-832-021-15	Sequence 15, Appl
420	15	1.9	5526	3	US-08-907-146-21	Sequence 21, Appl	c 493	15	1.9	246240	2	US-08-832-021-15	Sequence 15, Appl
421	15	1.9	5555	1	US-08-484-438-3	Sequence 3, Appli	c 494	15	1.9	246240	2	US-08-832-021-15	Sequence 15, Appl
422	15	1.9	5993	4	US-09-383-630-1	Sequence 2, Appli	c 495	14	1.8	14	3	US-08-724-466B-12	Sequence 12, Appl
423	15	1.9	5993	4	US-09-383-630-2	Sequence 2, Appli	c 496	14	1.8	14	3	US-08-882-164D-12	Sequence 12, Appl
424	15	1.9	6028	4	US-09-011-745-5	Sequence 8, Appli	c 497	14	1.8	15	3	US-08-832-021-49	Sequence 49, Appl
425	15	1.9	6350	2	US-08-385-345A-8	Sequence 8, Appli	c 498	14	1.8	15	3	US-08-832-021-50	Sequence 50, Appl
426	15	1.9	6370	4	US-09-245-041-12	Sequence 12, Appl	c 499	14	1.8	16	1	US-08-284-484A-4	Sequence 51, Appl
427	15	1.9	6639	1	US-08-727-034-1	Sequence 2, Appli	c 500	14	1.8	20	4	US-09-328-942-7	Sequence 7, Appli
428	15	1.9	6641	4	US-09-064-693A-25	Sequence 25, Appl	c 501	14	1.8	20	4	US-08-482-918-32	Sequence 32, Appl
429	15	1.9	6642	1	US-08-727-034-5	Sequence 5, Appli	c 502	14	1.8	20	4	US-09-224-681-32	Sequence 32, Appl
430	15	1.9	6669	3	US-09-212-971-5	Sequence 5, Appli	c 503	14	1.8	21	1	US-08-336-728A-32	Sequence 4, Appli
431	15	1.9	6669	3	US-08-800-929A-5	Sequence 5, Appli	c 504	14	1.8	21	2	US-08-128-011-4	Sequence 142, App
432	15	1.9	6669	4	US-09-617-053A-5	Sequence 5, Appli	c 505	14	1.8	21	2	US-08-403-888A-142	Sequence 146, App
433	15	1.9	6843	1	US-08-727-034-6	Sequence 6, Appli	c 506	14	1.8	22	1	US-08-235-180-23	Sequence 23, Appl
434	15	1.9	6911	1	US-08-311-174-4	Sequence 4, Appli	c 507	14	1.8	22	1	US-08-332-420-5	Sequence 5, Appli
435	15	1.9	6961	1	US-08-727-034-2	Sequence 2, Appli	c 508	14	1.8	22	3	US-08-974-180-1	Sequence 1, Appli
436	15	1.9	7070	1	US-08-619-554-3	Sequence 3, Appli	c 509	14	1.8	23	5	PCT-US94-05407-7	Sequence 8, Appli
437	15	1.9	7452	3	US-08-592-500-1	Sequence 1, Appli	c 510	14	1.8	23	5	PCT-US94-05407-8	Sequence 8, Appli
438	15	1.9	7452	3	US-08-195-006-1	Sequence 1, Appli	c 511	14	1.8	24	1	US-09-434-131A-6	Sequence 6, Appli
439	15	1.9	7452	5	PCT-US94-07644A-1	Sequence 1, Appli	c 512	14	1.8	25	1	US-08-683-877-5	Sequence 5, Appli
440	15	1.9	8083	4	US-09-383-630-4	Sequence 5, Appli	c 513	14	1.8	26	3	US-08-388-353-624	Sequence 624, App
441	15	1.9	8083	4	US-09-383-630-5	Sequence 6, Appli	c 514	14	1.8	26	3	US-08-488-551B-624	Sequence 624, App
442	15	1.9	8342	3	US-08-545-860D-63	Sequence 63, Appl	c 515	14	1.8	27	4	US-08-584-040-5169	Sequence 5169, Ap
443	15	1.9	8342	5	PCT-US94-04496-63	Sequence 63, Appl	c 516	14	1.8	27	4	US-08-584-040-5169	Sequence 5169, Ap
444	15	1.9	8387	2	US-08-532-814-1	Sequence 1, Appli	c 517	14	1.8	29	2	US-08-559-998-410	Sequence 410, App
445	15	1.9	8388	4	US-09-225-509-1	Sequence 14, Appl	c 518	14	1.8	30	4	US-09-225-928-410	Sequence 410, App
446	15	1.9	8589	4	US-09-245-041-14	Sequence 1, Appli	c 519	14	1.8	33	1	US-08-018-584A-114	Sequence 114, App
447	15	1.9	8827	4	US-09-245-041-1	Sequence 3, Appli	c 520	14	1.8	37	4	US-08-133-711-18	Sequence 18, Appl
448	15	1.9	8878	1	US-08-206-176-3	Sequence 3, Appli	c 521	14	1.8	37	4	US-08-434-131A-4	Sequence 4, Appli
449	15	1.9	9620	4	US-08-952-127-11	Sequence 11, Appl	c 522	14	1.8	40	2	US-09-306-290-4	Sequence 11, Appl
450	15	1.9	9934	4	US-08-977-171-2	Sequence 2, Appli	c 523	14	1.8	42	2	US-08-484-575A-11	Sequence 11, Appl
451	15	1.9	10718	3	US-08-325-426B-1	Sequence 21, Appl	c 524	14	1.8	42	3	US-08-477-459-11	Sequence 11, Appl
452	15	1.9	10815	4	US-09-004-838-21	Sequence 1, Appli	c 525	14	1.8	42	3	US-08-479-869-11	Sequence 11, Appl
453	15	1.9	11288	4	US-08-646-301A-1	Sequence 1, Appli	c 526	14	1.8	42	3	US-08-486-414-11	Sequence 11, Appl
454	15	1.9	11288	4	US-08-481-968A-4	Sequence 4, Appli	c 527	14	1.8	42	5	PCT-US94-01826A-11	Sequence 11, Appl
455	15	1.9	11288	4	US-08-154-712B-4	Sequence 4, Appli	c 528	14	1.8	42	5	PCT-US94-02252A-11	Sequence 11, Appl
456	15	1.9	11461	3	US-08-669-161A-29	Sequence 29, Appl	c 529	14	1.8	46	1	US-08-232-463-40	Sequence 40, Appl
457	15	1.9	13149	4	US-09-004-838-87	Sequence 87, Appl	c 530	14	1.8	46	5	PCT-US91-02954-9	Sequence 9, Appli
458	15	1.9	14796	4	US-08-975-080-35	Sequence 35, Appl	c 531	14	1.8	46	5	PCT-US94-05407-3	Sequence 3, Appli
459	15	1.9	14796	4	US-09-630-706-10	Sequence 10, Appl	c 532	14	1.8	46	5	PCT-US94-05407-10	Sequence 10, Appl
460	15	1.9	14796	4	US-09-496-694B-3	Sequence 3, Appli	c 533	14	1.8	47	4	US-09-338-907-273	Sequence 273, App
461	15	1.9	15144	3	US-08-458-434A-6	Sequence 6, Appli	c 534	14	1.8	47	4	US-09-218-207-273	Sequence 273, App
462	15	1.9	17056	4	US-09-245-041-3	Sequence 3, Appli	c 535	14	1.8	49	3	US-08-651-472-70	Sequence 70, Appl
463	15	1.9	17410	1	US-07-841-646-3	Sequence 3, Appli	c 536	14	1.8	49	4	US-08-358-928-70	Sequence 70, Appl
464	15	1.9	17410	1	US-08-147-023-3	Sequence 3, Appli	c 537	14	1.8	49	5	PCT-US96-07709-39	Sequence 39, Appl
465	15	1.9	17410	1	US-08-447-570-3	Sequence 3, Appli	c 538	14	1.8	49	5	PCT-US96-07709-40	Sequence 40, Appl

c 539	14	1.8	49	5	PCT-US96-09848-19	Sequence 19, Appl	c 612	14	1.8	108	4	US-08-375-992A-32	Sequence 32, Appl
c 540	14	1.8	49	5	PCT-US96-09848-20	Sequence 20, Appl	c 613	14	1.8	108	5	PCT-US93-00324-32	Sequence 32, Appl
c 541	14	1.8	51	3	US-08-651-472-56	Sequence 56, Appl	c 614	14	1.8	110	2	US-08-602-093-19	Sequence 19, Appl
c 542	14	1.8	51	3	US-08-358-928-56	Sequence 56, Appl	c 615	14	1.8	111	2	US-08-097-554A-78	Sequence 78, Appl
c 543	14	1.8	53	3	US-08-651-472-57	Sequence 57, Appl	c 616	14	1.8	111	2	US-08-912-129A-6	Sequence 6, Appl
c 544	14	1.8	53	4	US-08-358-928-57	Sequence 57, Appl	c 617	14	1.8	111	2	US-08-035-648-13	Sequence 13, Appl
c 545	14	1.8	54	4	US-08-584-040-8265	Sequence 8265, Ap	c 618	14	1.8	114	3	US-09-001-951-13	Sequence 13, Appl
c 546	14	1.8	55	1	US-07-803-633A-3	Sequence 3, Appl	c 619	14	1.8	114	3	US-08-480-640A-78	Sequence 78, Appl
c 547	14	1.8	55	1	US-07-803-633A-4	Sequence 4, Appl	c 620	14	1.8	117	3	US-08-295-802-78	Sequence 78, Appl
c 548	14	1.8	55	1	US-07-750-080A-38	Sequence 38, Appl	c 621	14	1.8	117	3	US-08-686-968C-130	Sequence 130, App
c 549	14	1.8	55	2	US-07-750-080A-39	Sequence 39, Appl	c 622	14	1.8	117	4	US-08-686-968C-144	Sequence 144, App
c 550	14	1.8	55	2	US-08-525-742-13	Sequence 14, Appl	c 623	14	1.8	117	4	US-08-488-237A-78	Sequence 78, Appl
c 551	14	1.8	55	2	US-08-525-742-14	Sequence 14, Appl	c 624	14	1.8	117	4	US-08-375-992A-78	Sequence 86, Appl
c 552	14	1.8	55	3	US-08-651-472-38	Sequence 38, Appl	c 625	14	1.8	119	2	US-08-097-554A-86	Sequence 86, Appl
c 553	14	1.8	55	3	US-08-651-472-39	Sequence 38, Appl	c 626	14	1.8	119	2	US-08-097-554A-95	Sequence 95, Appl
c 554	14	1.8	55	4	US-08-358-928-38	Sequence 38, Appl	c 627	14	1.8	119	2	US-08-659-251-49	Sequence 49, Appl
c 555	14	1.8	55	4	US-08-358-928-39	Sequence 39, Appl	c 628	14	1.8	119	2	US-08-659-251-49	Sequence 49, Appl
c 556	14	1.8	56	2	US-08-776-944-9	Sequence 9, Appl	c 629	14	1.8	119	4	US-09-256-490-49	Sequence 49, Appl
c 557	14	1.8	59	4	US-08-952-793-236	Sequence 236, App	c 630	14	1.8	120	5	PCT-US96-11445-49	Sequence 151, App
c 558	14	1.8	59	5	PCT-US96-09455A-236	Sequence 236, App	c 631	14	1.8	120	5	PCT-US96-11445-49	Sequence 151, App
c 559	14	1.8	60	4	US-09-396-281-8	Sequence 8, Appl	c 632	14	1.8	123	4	US-08-686-968C-151	Sequence 140, App
c 560	14	1.8	61	2	US-09-032-684-6	Sequence 6, Appl	c 633	14	1.8	123	4	US-08-686-968C-140	Sequence 86, Appl
c 561	14	1.8	63	1	US-08-232-463-47	Sequence 8, Appl	c 634	14	1.8	124	3	US-08-480-640A-86	Sequence 95, Appl
c 562	14	1.8	69	4	US-09-269-911A-8	Sequence 43, Appl	c 635	14	1.8	124	3	US-08-480-640A-95	Sequence 86, Appl
c 563	14	1.8	70	2	US-08-097-554A-43	Sequence 43, Appl	c 636	14	1.8	124	4	US-08-295-802-86	Sequence 95, Appl
c 564	14	1.8	70	3	US-08-480-640A-43	Sequence 43, Appl	c 637	14	1.8	124	4	US-08-488-237A-86	Sequence 86, Appl
c 565	14	1.8	70	3	US-08-295-802-43	Sequence 43, Appl	c 638	14	1.8	124	4	US-08-375-992A-86	Sequence 86, Appl
c 566	14	1.8	70	4	US-08-488-237A-43	Sequence 43, Appl	c 639	14	1.8	124	4	US-08-375-992A-95	Sequence 95, Appl
c 567	14	1.8	70	4	US-08-375-992A-43	Sequence 43, Appl	c 640	14	1.8	127	1	US-07-750-080A-13	Sequence 13, Appl
c 568	14	1.8	74	2	US-08-097-554A-44	Sequence 44, Appl	c 641	14	1.8	127	3	US-08-480-640A-160	Sequence 160, App
c 569	14	1.8	74	3	US-08-480-640A-44	Sequence 44, Appl	c 642	14	1.8	127	3	US-08-651-472-13	Sequence 13, Appl
c 570	14	1.8	74	3	US-08-295-802-44	Sequence 44, Appl	c 643	14	1.8	127	3	US-08-295-802-160	Sequence 160, App
c 571	14	1.8	74	4	US-08-488-237A-44	Sequence 44, Appl	c 644	14	1.8	127	4	US-08-488-237A-160	Sequence 13, Appl
c 572	14	1.8	74	4	US-08-375-992A-44	Sequence 44, Appl	c 645	14	1.8	127	4	US-08-358-928-13	Sequence 160, App
c 573	14	1.8	80	1	US-07-920-281C-25	Sequence 25, Appl	c 646	14	1.8	127	4	US-08-375-992A-160	Sequence 160, App
c 574	14	1.8	80	2	US-08-466-277-50	Sequence 25, Appl	c 647	14	1.8	128	3	US-08-480-640A-145	Sequence 145, App
c 575	14	1.8	86	2	US-08-525-742-50	Sequence 50, Appl	c 648	14	1.8	128	3	US-08-295-802-145	Sequence 145, App
c 576	14	1.8	88	1	US-07-750-080A-11	Sequence 11, Appl	c 649	14	1.8	128	4	US-08-488-237A-145	Sequence 145, App
c 577	14	1.8	88	3	US-08-651-472-11	Sequence 11, Appl	c 650	14	1.8	128	4	US-08-375-992A-145	Sequence 145, App
c 578	14	1.8	88	4	US-08-358-928-11	Sequence 11, Appl	c 651	14	1.8	133	3	US-08-480-640A-176	Sequence 176, App
c 579	14	1.8	91	2	US-08-525-742-51	Sequence 51, Appl	c 652	14	1.8	133	3	US-08-295-802-176	Sequence 176, App
c 580	14	1.8	92	1	US-07-750-080A-12	Sequence 12, Appl	c 653	14	1.8	133	4	US-08-488-237A-176	Sequence 176, App
c 581	14	1.8	92	3	US-08-651-472-12	Sequence 12, Appl	c 654	14	1.8	133	4	US-08-375-992A-176	Sequence 176, App
c 582	14	1.8	92	4	US-08-358-928-12	Sequence 12, Appl	c 655	14	1.8	134	1	US-07-750-080A-14	Sequence 14, Appl
c 583	14	1.8	93	1	US-07-750-080A-40	Sequence 40, Appl	c 656	14	1.8	134	3	US-08-651-472-14	Sequence 14, Appl
c 584	14	1.8	93	3	US-08-525-742-28	Sequence 28, Appl	c 657	14	1.8	134	4	US-08-358-928-14	Sequence 14, Appl
c 585	14	1.8	93	3	US-08-651-472-28	Sequence 28, Appl	c 658	14	1.8	137	2	US-08-486-414-37	Sequence 22, Appl
c 586	14	1.8	93	4	US-08-358-928-40	Sequence 40, Appl	c 659	14	1.8	137	3	US-08-486-414-37	Sequence 37, Appl
c 587	14	1.8	95	2	US-08-525-742-29	Sequence 29, Appl	c 660	14	1.8	138	3	US-08-480-640A-198	Sequence 198, App
c 588	14	1.8	96	2	US-08-525-742-30	Sequence 30, Appl	c 661	14	1.8	138	4	US-08-686-968C-203	Sequence 203, App
c 589	14	1.8	97	1	US-07-750-080A-41	Sequence 41, Appl	c 662	14	1.8	138	4	US-08-488-237A-198	Sequence 198, App
c 590	14	1.8	97	2	US-08-525-742-27	Sequence 27, Appl	c 663	14	1.8	138	4	US-08-375-992A-198	Sequence 181, App
c 591	14	1.8	97	3	US-08-525-742-27	Sequence 27, Appl	c 664	14	1.8	138	4	US-08-488-237A-181	Sequence 181, App
c 592	14	1.8	97	4	US-08-651-472-41	Sequence 41, Appl	c 665	14	1.8	140	3	US-08-295-802-181	Sequence 181, App
c 593	14	1.8	97	4	US-08-358-928-41	Sequence 41, Appl	c 666	14	1.8	140	3	US-08-488-237A-181	Sequence 181, App
c 594	14	1.8	97	5	US-08-952-793-205	Sequence 205, App	c 667	14	1.8	140	4	US-08-488-237A-181	Sequence 181, App
c 595	14	1.8	98	4	PCT-US96-09455A-205	Sequence 205, App	c 668	14	1.8	141	3	US-08-375-992A-203	Sequence 203, App
c 596	14	1.8	98	4	US-08-991-789A-282	Sequence 282, App	c 669	14	1.8	141	3	US-08-480-640A-203	Sequence 198, App
c 597	14	1.8	102	4	US-09-062-451-282	Sequence 10, Appl	c 670	14	1.8	141	4	US-08-686-968C-198	Sequence 198, App
c 598	14	1.8	102	2	US-07-820-154A-10	Sequence 10, Appl	c 671	14	1.8	141	4	US-08-488-237A-203	Sequence 203, App
c 599	14	1.8	102	2	US-08-097-554A-10	Sequence 10, Appl	c 672	14	1.8	141	4	US-08-375-992A-203	Sequence 203, App
c 600	14	1.8	102	3	US-08-480-640A-10	Sequence 10, Appl	c 673	14	1.8	150	4	US-09-439-313-320	Sequence 320, App
c 601	14	1.8	102	3	US-08-295-802-10	Sequence 10, Appl	c 674	14	1.8	153	2	US-08-484-575A-27	Sequence 27, Appl
c 602	14	1.8	102	4	US-08-686-968C-106	Sequence 106, App	c 675	14	1.8	153	4	US-08-486-414-42	Sequence 42, Appl
c 603	14	1.8	102	4	US-08-991-789A-272	Sequence 272, App	c 676	14	1.8	156	4	US-09-019-095A-41	Sequence 41, Appl
c 604	14	1.8	102	4	US-08-488-237A-10	Sequence 10, Appl	c 677	14	1.8	162	3	US-08-746-411A-3	Sequence 3, Appl
c 605	14	1.8	102	4	US-08-375-992A-10	Sequence 10, Appl	c 678	14	1.8	168	3	US-08-480-640A-150	Sequence 150, App
c 606	14	1.8	102	5	US-09-062-451-272	Sequence 10, Appl	c 679	14	1.8	168	3	US-08-295-802-150	Sequence 150, App
c 607	14	1.8	108	1	PCT-US93-00324-10	Sequence 10, Appl	c 680	14	1.8	168	4	US-08-686-968C-120	Sequence 120, App
c 608	14	1.8	108	2	US-07-820-154A-32	Sequence 32, Appl	c 681	14	1.8	168	4	US-08-488-237A-120	Sequence 120, App
c 609	14	1.8	108	3	US-08-097-554A-32	Sequence 32, Appl	c 682	14	1.8	168	4	US-08-488-237A-150	Sequence 150, App
c 610	14	1.8	108	3	US-08-480-640A-32	Sequence 32, Appl	c 683	14	1.8	177	4	US-08-375-992A-150	Sequence 150, App
c 611	14	1.8	108	4	US-08-295-802-32	Sequence 32, Appl	c 684	14	1.8	178	2	US-08-686-968C-147	Sequence 147, App
					US-08-488-237A-32	Sequence 32, Appl						US-08-484-575A-16	Sequence 16, Appl

c 685	14	1.8	178	3	US-08-477-459-16	Sequence 16, Appl	c 758	14	1.8	300	2	US-09-032-684-17	Sequence 17, Appl
c 686	14	1.8	178	3	US-08-479-869-16	Sequence 16, Appl	c 759	14	1.8	302	1	US-08-189-199A-1	Sequence 1, Appl
c 687	14	1.8	178	3	US-08-486-414-16	Sequence 16, Appl	c 760	14	1.8	304	1	US-08-358-171-23	Sequence 23, Appl
c 688	14	1.8	178	5	PCT-US94-01826A-16	Sequence 16, Appl	c 761	14	1.8	308	3	US-09-090-947-23	Sequence 23, Appl
c 689	14	1.8	178	5	PCT-US94-02252A-16	Sequence 16, Appl	c 762	14	1.8	308	3	US-09-035-648-16	Sequence 16, Appl
c 690	14	1.8	180	2	US-08-097-554A-72	Sequence 72, Appl	c 763	14	1.8	308	4	US-09-001-951-16	Sequence 16, Appl
c 691	14	1.8	180	3	US-08-480-640A-72	Sequence 72, Appl	c 764	14	1.8	313	3	US-08-398-633-8	Sequence 8, Appl
c 692	14	1.8	180	3	US-08-295-802-72	Sequence 72, Appl	c 765	14	1.8	314	4	US-08-976-259-41	Sequence 41, Appl
c 693	14	1.8	180	4	US-08-686-968C-116	Sequence 116, App	c 766	14	1.8	315	4	US-08-945-424-1	Sequence 1, Appl
c 694	14	1.8	180	4	US-08-488-237A-72	Sequence 72, Appl	c 767	14	1.8	322	4	US-09-385-982-216	Sequence 216, App
c 695	14	1.8	180	4	US-08-375-992A-72	Sequence 72, Appl	c 768	14	1.8	322	4	US-09-385-982-362	Sequence 362, App
c 696	14	1.8	182	2	US-08-097-554A-64	Sequence 64, Appl	c 769	14	1.8	326	3	US-09-035-648-9	Sequence 9, Appl
c 697	14	1.8	182	2	US-08-484-575A-15	Sequence 15, App	c 770	14	1.8	326	3	US-09-001-951-9	Sequence 9, Appl
c 698	14	1.8	182	3	US-08-477-459-15	Sequence 15, Appl	c 771	14	1.8	327	3	US-08-766-355-9	Sequence 9, Appl
c 699	14	1.8	182	3	US-08-480-640A-64	Sequence 64, Appl	c 772	14	1.8	327	4	US-09-385-982-544	Sequence 544, App
c 700	14	1.8	182	3	US-08-479-869-15	Sequence 15, Appl	c 773	14	1.8	327	4	US-09-003-198A-9	Sequence 9, Appl
c 701	14	1.8	182	3	US-08-295-802-64	Sequence 64, Appl	c 774	14	1.8	327	4	US-09-428-805-9	Sequence 9, Appl
c 702	14	1.8	182	3	US-08-486-414-15	Sequence 15, App	c 775	14	1.8	333	4	US-09-018-584A-27	Sequence 27, Appl
c 703	14	1.8	182	4	US-08-991-789A-289	Sequence 289, App	c 776	14	1.8	336	2	US-08-691-814B-96	Sequence 96, Appl
c 704	14	1.8	182	4	US-08-488-237A-64	Sequence 64, Appl	c 777	14	1.8	342	4	US-09-385-982-342	Sequence 342, App
c 705	14	1.8	182	4	US-08-375-992A-64	Sequence 64, Appl	c 778	14	1.8	348	1	US-08-686-878A-54	Sequence 54, Appl
c 706	14	1.8	182	4	US-09-062-451-289	Sequence 289, App	c 779	14	1.8	348	2	US-08-721-924-4	Sequence 4, Appl
c 707	14	1.8	182	5	PCT-US94-01826A-15	Sequence 15, Appl	c 780	14	1.8	348	4	US-09-385-982-283	Sequence 283, App
c 708	14	1.8	182	5	PCT-US94-02252A-15	Sequence 15, App	c 781	14	1.8	348	4	US-09-175-928-8	Sequence 8, Appl
c 709	14	1.8	185	3	US-08-480-640A-156	Sequence 156, App	c 782	14	1.8	349	3	US-09-087-194-37	Sequence 37, Appl
c 710	14	1.8	185	3	US-08-295-802-156	Sequence 156, App	c 783	14	1.8	352	4	US-09-385-982-529	Sequence 529, App
c 711	14	1.8	185	4	US-08-488-237A-156	Sequence 156, App	c 784	14	1.8	374	2	US-08-370-156-24	Sequence 24, Appl
c 712	14	1.8	185	4	US-08-375-992A-156	Sequence 156, App	c 785	14	1.8	374	4	US-09-385-982-135	Sequence 135, App
c 713	14	1.8	186	4	US-08-686-968C-132	Sequence 132, App	c 786	14	1.8	380	4	US-09-385-982-457	Sequence 457, App
c 714	14	1.8	186	4	US-08-686-968C-137	Sequence 137, App	c 787	14	1.8	382	3	US-09-035-648-10	Sequence 10, Appl
c 715	14	1.8	186	4	US-08-686-968C-154	Sequence 154, App	c 788	14	1.8	382	4	US-09-001-951-10	Sequence 10, Appl
c 716	14	1.8	187	3	US-09-094-287-7	Sequence 7, Appl	c 789	14	1.8	390	4	US-08-905-223-98	Sequence 98, Appl
c 717	14	1.8	189	4	US-09-113-750A-29	Sequence 29, Appl	c 790	14	1.8	400	2	US-08-244-537-3	Sequence 3, Appl
c 718	14	1.8	191	2	US-09-032-684-4	Sequence 4, Appl	c 791	14	1.8	403	3	US-09-035-648-3	Sequence 3, Appl
c 719	14	1.8	193	3	US-08-480-640A-171	Sequence 171, App	c 792	14	1.8	403	4	US-09-385-982-29	Sequence 29, Appl
c 720	14	1.8	193	3	US-08-295-802-171	Sequence 171, App	c 793	14	1.8	403	4	US-09-001-951-3	Sequence 3, Appl
c 721	14	1.8	193	4	US-08-752-540-6	Sequence 6, Appl	c 794	14	1.8	404	4	US-09-386-493-5	Sequence 5, Appl
c 722	14	1.8	193	4	US-08-488-237A-171	Sequence 171, App	c 795	14	1.8	405	1	US-08-469-427A-8	Sequence 8, Appl
c 723	14	1.8	193	4	US-08-375-992A-171	Sequence 171, App	c 796	14	1.8	405	2	US-08-609-443B-8	Sequence 8, Appl
c 724	14	1.8	198	3	US-09-035-648-5	Sequence 5, Appl	c 797	14	1.8	405	2	US-08-569-063C-8	Sequence 8, Appl
c 725	14	1.8	198	4	US-08-686-968C-125	Sequence 125, App	c 798	14	1.8	405	4	US-09-020-956-101	Sequence 101, App
c 726	14	1.8	198	4	US-09-001-951-5	Sequence 5, Appl	c 799	14	1.8	405	4	US-09-030-607-101	Sequence 101, App
c 727	14	1.8	201	4	US-09-113-750A-28	Sequence 28, Appl	c 800	14	1.8	405	4	US-09-439-313-101	Sequence 101, App
c 728	14	1.8	206	1	US-07-820-154A-21	Sequence 21, Appl	c 801	14	1.8	411	4	US-09-385-982-5	Sequence 5, Appl
c 729	14	1.8	206	2	US-08-097-554A-21	Sequence 21, Appl	c 802	14	1.8	419	4	US-09-030-607-201	Sequence 201, App
c 730	14	1.8	206	3	US-08-480-640A-21	Sequence 21, Appl	c 803	14	1.8	419	4	US-09-439-313-201	Sequence 201, App
c 731	14	1.8	206	3	US-08-295-802-21	Sequence 21, Appl	c 804	14	1.8	421	3	US-08-983-409-2	Sequence 2, Appl
c 732	14	1.8	206	4	US-08-686-968C-111	Sequence 111, App	c 805	14	1.8	425	2	US-08-967-101-102	Sequence 102, App
c 733	14	1.8	206	4	US-08-488-237A-21	Sequence 21, Appl	c 806	14	1.8	425	2	US-08-592-541-102	Sequence 102, App
c 734	14	1.8	206	4	US-08-375-992A-21	Sequence 21, Appl	c 807	14	1.8	425	3	US-09-124-698-102	Sequence 102, App
c 735	14	1.8	206	5	PCT-US93-00324-21	Sequence 21, Appl	c 808	14	1.8	425	4	US-09-127-480-102	Sequence 102, App
c 736	14	1.8	213	3	US-08-513-974B-37	Sequence 37, Appl	c 809	14	1.8	425	4	US-08-496-841C-102	Sequence 102, App
c 737	14	1.8	218	3	US-09-035-648-14	Sequence 14, Appl	c 810	14	1.8	426	2	US-08-975-316-52	Sequence 52, Appl
c 738	14	1.8	218	4	US-09-001-951-14	Sequence 14, Appl	c 811	14	1.8	430	4	US-08-991-789A-250	Sequence 250, App
c 739	14	1.8	219	4	US-08-991-789A-286	Sequence 286, App	c 812	14	1.8	430	4	US-09-062-451-250	Sequence 250, App
c 740	14	1.8	219	4	US-09-062-451-286	Sequence 286, App	c 813	14	1.8	431	4	US-08-991-789A-281	Sequence 281, App
c 741	14	1.8	231	4	US-09-439-313-463	Sequence 463, App	c 814	14	1.8	431	4	US-09-062-451-281	Sequence 281, App
c 742	14	1.8	234	1	US-08-840-683-3	Sequence 3, Appl	c 815	14	1.8	436	1	US-08-181-271A-41	Sequence 41, Appl
c 743	14	1.8	234	2	US-08-555-722-3	Sequence 3, Appl	c 816	14	1.8	436	1	US-08-449-315-41	Sequence 41, Appl
c 744	14	1.8	234	3	US-09-384-301-3	Sequence 318, App	c 817	14	1.8	436	1	US-08-444-803-41	Sequence 41, Appl
c 745	14	1.8	240	3	US-08-513-974B-318	Sequence 318, App	c 818	14	1.8	436	1	US-08-449-043-41	Sequence 41, Appl
c 746	14	1.8	249	3	US-08-480-640A-209	Sequence 209, App	c 819	14	1.8	436	1	US-08-456-265A-41	Sequence 41, Appl
c 747	14	1.8	249	4	US-08-686-968C-209	Sequence 209, App	c 820	14	1.8	436	1	US-08-455-416-41	Sequence 41, Appl
c 748	14	1.8	249	4	US-08-488-237A-209	Sequence 209, App	c 821	14	1.8	436	1	US-08-455-244-41	Sequence 41, Appl
c 749	14	1.8	249	4	US-08-375-992A-209	Sequence 209, App	c 822	14	1.8	436	1	US-08-454-876-41	Sequence 41, Appl
c 750	14	1.8	255	1	US-08-487-748A-2	Sequence 2, Appl	c 823	14	1.8	436	2	US-08-457-364-41	Sequence 41, Appl
c 751	14	1.8	255	3	US-08-398-633-2	Sequence 2, Appl	c 824	14	1.8	436	2	US-08-456-262-41	Sequence 41, Appl
c 752	14	1.8	255	3	US-08-480-070C-2	Sequence 2, Appl	c 825	14	1.8	436	2	US-08-456-240-41	Sequence 41, Appl
c 753	14	1.8	255	3	US-08-829-525-2	Sequence 2, Appl	c 826	14	1.8	436	2	US-08-455-736-41	Sequence 41, Appl
c 754	14	1.8	255	4	US-08-609-583A-2	Sequence 2, Appl	c 827	14	1.8	436	2	US-08-971-217-41	Sequence 41, Appl
c 755	14	1.8	255	4	US-08-937-393-2	Sequence 2, Appl	c 828	14	1.8	436	3	US-08-821-451A-3	Sequence 3, Appl
c 756	14	1.8	256	4	US-09-385-982-187	Sequence 187, App	c 829	14	1.8	436	4	US-09-263-810-3	Sequence 3, Appl
c 757	14	1.8	296	4	US-09-385-982-19	Sequence 19, Appl	c 830	14	1.8	436	4	US-09-350-600-41	Sequence 41, Appl

831	14	1.8	436	4	US-09-583-169-3	Sequence 3, Appl	904	14	1.8	584	4	US-09-347-801-11	Sequence 11, Appl
832	14	1.8	437	4	US-09-091-725-46	Sequence 46, Appl	905	14	1.8	585	2	US-08-882-704A-1	Sequence 1, Appl
c 833	14	1.8	440	2	US-08-967-101-105	Sequence 105, App	906	14	1.8	586	1	US-08-463-115-75	Sequence 75, Appl
c 834	14	1.8	440	2	US-08-552-341-105	Sequence 105, App	907	14	1.8	586	1	US-08-465-388-75	Sequence 75, Appl
c 835	14	1.8	440	3	US-09-124-698-105	Sequence 105, App	c 908	14	1.8	588	3	US-08-965-504B-1	Sequence 1, Appl
c 836	14	1.8	440	4	US-09-127-480-105	Sequence 105, App	909	14	1.8	591	1	US-08-090-523-24	Sequence 24, Appl
c 837	14	1.8	440	4	US-08-496-841C-105	Sequence 105, App	910	14	1.8	591	1	US-08-334-639-3	Sequence 3, Appl
c 838	14	1.8	450	2	US-08-967-101-7	Sequence 7, Appl	911	14	1.8	591	1	US-08-398-627-24	Sequence 24, Appl
c 839	14	1.8	450	2	US-08-592-541-7	Sequence 7, Appl	912	14	1.8	591	1	US-08-406-858-25	Sequence 25, Appl
c 840	14	1.8	450	3	US-09-124-698-7	Sequence 7, Appl	c 913	14	1.8	591	5	US-09-385-982-406	Sequence 406, pp
c 841	14	1.8	450	4	US-09-127-480-7	Sequence 7, Appl	914	14	1.8	591	5	PCT-US94-05275-25	Sequence 25, Appl
c 842	14	1.8	450	4	US-08-496-841C-7	Sequence 7, Appl	915	14	1.8	593	1	US-08-443-568B-13	Sequence 13, Appl
c 843	14	1.8	455	4	US-08-991-789A-273	Sequence 273, App	c 916	14	1.8	593	4	US-09-385-982-448	Sequence 448, App
c 844	14	1.8	455	4	US-09-062-451-273	Sequence 273, App	917	14	1.8	593	5	PCT-US94-06997-13	Sequence 13, Appl
c 845	14	1.8	461	4	US-08-991-789A-274	Sequence 274, App	918	14	1.8	602	4	US-09-040-984-11	Sequence 11, Appl
c 846	14	1.8	461	4	US-09-062-451-274	Sequence 274, App	919	14	1.8	602	4	US-09-123-912-11	Sequence 11, Appl
c 847	14	1.8	468	3	US-08-600-982-29	Sequence 29, Appl	920	14	1.8	603	2	US-08-924-838-6	Sequence 6, Appl
c 848	14	1.8	468	5	PCT-US94-10261A-29	Sequence 29, Appl	c 921	14	1.8	604	4	US-09-385-982-496	Sequence 496, App
c 849	14	1.8	470	4	US-09-020-956-102	Sequence 102, App	922	14	1.8	606	1	US-08-592-126-99	Sequence 99, Appl
c 850	14	1.8	470	4	US-09-030-607-102	Sequence 102, App	923	14	1.8	606	4	US-09-040-984-55	Sequence 55, Appl
c 851	14	1.8	470	4	US-09-439-313-102	Sequence 102, App	c 924	14	1.8	606	4	US-09-064-414-1	Sequence 1, Appl
c 852	14	1.8	475	4	US-09-328-111-432	Sequence 432, App	c 925	14	1.8	606	4	US-09-064-414-3	Sequence 3, Appl
c 853	14	1.8	475	1	US-08-324-243-37	Sequence 37, Appl	926	14	1.8	606	4	US-09-123-912-55	Sequence 55, Appl
c 854	14	1.8	485	1	US-08-532-390-37	Sequence 37, Appl	c 927	14	1.8	608	4	US-09-385-982-183	Sequence 183, App
c 855	14	1.8	485	3	US-08-717-324-37	Sequence 37, Appl	c 928	14	1.8	608	4	US-09-385-982-523	Sequence 523, App
c 856	14	1.8	485	5	PCT-US95-11511-37	Sequence 37, Appl	c 929	14	1.8	611	4	US-09-385-982-178	Sequence 178, App
c 857	14	1.8	490	4	US-09-003-198A-19	Sequence 19, Appl	c 930	14	1.8	613	4	US-09-385-982-144	Sequence 144, App
c 858	14	1.8	491	1	US-08-133-711-40	Sequence 40, Appl	931	14	1.8	614	4	US-09-385-982-255	Sequence 255, App
c 859	14	1.8	496	4	US-09-328-111-125	Sequence 125, App	932	14	1.8	615	4	US-09-385-982-240	Sequence 240, App
c 860	14	1.8	500	2	US-09-018-595B-3	Sequence 3, Appl	933	14	1.8	618	4	US-09-385-982-218	Sequence 218, App
c 861	14	1.8	500	3	US-09-324-709A-3	Sequence 3, Appl	c 934	14	1.8	619	4	US-09-328-111-829	Sequence 829, App
c 862	14	1.8	501	3	US-08-699-628-1	Sequence 1, Appl	c 935	14	1.8	622	4	US-09-385-982-184	Sequence 184, App
c 863	14	1.8	501	4	US-09-339-913B-96	Sequence 96, Appl	c 936	14	1.8	622	4	US-09-385-982-312	Sequence 312, App
c 864	14	1.8	501	4	US-09-339-904A-96	Sequence 96, Appl	937	14	1.8	623	4	US-08-905-223-25	Sequence 23, Appl
c 865	14	1.8	501	4	US-08-769-062B-96	Sequence 96, Appl	c 938	14	1.8	624	4	US-09-385-982-359	Sequence 359, App
c 866	14	1.8	501	4	US-09-344-002B-96	Sequence 96, Appl	c 939	14	1.8	626	4	US-09-385-982-39	Sequence 39, Appl
c 867	14	1.8	506	1	US-08-398-617-13	Sequence 13, Appl	940	14	1.8	626	4	US-09-064-414-5	Sequence 5, Appl
c 868	14	1.8	506	2	US-08-398-615-13	Sequence 13, Appl	c 941	14	1.8	627	4	US-09-385-982-305	Sequence 305, App
c 869	14	1.8	506	3	US-08-397-303-13	Sequence 10, Appl	c 942	14	1.8	628	4	US-09-385-982-354	Sequence 354, App
c 870	14	1.8	507	3	US-08-766-355-10	Sequence 10, Appl	c 943	14	1.8	631	4	US-09-328-111-126	Sequence 126, App
c 871	14	1.8	507	4	US-09-003-198A-10	Sequence 10, Appl	c 944	14	1.8	631	4	US-09-385-982-354	Sequence 354, App
c 872	14	1.8	507	4	US-09-428-805-10	Sequence 10, Appl	c 945	14	1.8	632	4	US-09-328-111-798	Sequence 798, App
c 873	14	1.8	509	4	US-09-030-607-202	Sequence 202, App	c 946	14	1.8	632	4	US-09-385-982-499	Sequence 499, App
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c 875	14	1.8	515	3	US-08-545-809A-63	Sequence 63, Appl	948	14	1.8	634	2	US-08-222-719-15	Sequence 15, Appl
c 876	14	1.8	515	4	US-09-439-313-472	Sequence 472, App	949	14	1.8	634	2	US-08-470-925-15	Sequence 15, Appl
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c 878	14	1.8	517	2	US-08-910-075-1	Sequence 1, Appl	951	14	1.8	634	5	PCT-US93-10443-15	Sequence 15, Appl
c 879	14	1.8	517	2	US-08-905-801A-1	Sequence 1, Appl	952	14	1.8	636	2	US-08-284-941-3	Sequence 3, Appl
c 880	14	1.8	528	1	US-08-422-613-1	Sequence 1, Appl	953	14	1.8	636	2	US-08-447-642-3	Sequence 3, Appl
c 881	14	1.8	532	3	US-09-036-113-1	Sequence 1, Appl	954	14	1.8	636	2	US-09-236-503-3	Sequence 3, Appl
c 882	14	1.8	535	3	US-09-094-287-8	Sequence 8, Appl	955	14	1.8	636	5	PCT-US93-02147A-3	Sequence 3, Appl
c 883	14	1.8	540	2	US-08-448-561-3	Sequence 3, Appl	c 956	14	1.8	647	4	US-08-927-219-44	Sequence 44, Appl
c 884	14	1.8	550	4	US-08-998-416-148	Sequence 148, App	957	14	1.8	651	2	US-08-912-129A-57	Sequence 57, Appl
c 885	14	1.8	552	4	US-09-020-956-79	Sequence 79, App	958	14	1.8	654	4	US-09-040-984-31	Sequence 31, Appl
c 886	14	1.8	552	4	US-09-030-607-79	Sequence 79, App	959	14	1.8	654	4	US-09-123-912-31	Sequence 31, Appl
c 887	14	1.8	552	4	US-09-439-313-79	Sequence 79, App	c 960	14	1.8	654	5	PCT-US91-02954-10	Sequence 10, Appl
c 888	14	1.8	557	4	US-09-385-982-395	Sequence 395, App	c 961	14	1.8	657	4	US-09-385-982-91	Sequence 91, Appl
c 889	14	1.8	558	4	US-09-030-607-181	Sequence 181, App	c 962	14	1.8	658	4	US-09-328-111-816	Sequence 816, App
c 890	14	1.8	558	4	US-09-439-313-181	Sequence 181, App	963	14	1.8	660	1	US-08-555-678-41	Sequence 41, Appl
c 891	14	1.8	564	1	US-08-117-362-32	Sequence 32, App	964	14	1.8	663	4	US-08-623-428D-6	Sequence 6, Appl
c 892	14	1.8	564	1	US-08-486-924-32	Sequence 32, App	c 965	14	1.8	669	4	US-09-328-111-782	Sequence 782, App
c 893	14	1.8	566	4	US-09-328-111-466	Sequence 466, App	c 966	14	1.8	675	4	US-08-998-416-1096	Sequence 1096, App
c 894	14	1.8	570	1	US-07-822-966B-1	Sequence 1, Appl	c 967	14	1.8	683	4	US-09-328-111-168	Sequence 168, App
c 895	14	1.8	571	1	US-08-322-742-14	Sequence 14, Appl	c 968	14	1.8	685	4	US-09-227-357-66	Sequence 66, Appl
c 896	14	1.8	578	4	US-09-328-111-757	Sequence 757, App	969	14	1.8	685	4	US-09-227-357-100	Sequence 100, App
c 897	14	1.8	580	2	US-08-809-763-2	Sequence 2, Appl	c 970	14	1.8	688	6	5498694-3	Patent No. 5498694
c 898	14	1.8	580	3	US-08-956-253-2	Sequence 2, Appl	c 971	14	1.8	690	4	US-09-328-111-74	Sequence 74, Appl
c 899	14	1.8	581	1	US-07-620-426B-30	Sequence 30, Appl	972	14	1.8	704	4	US-09-132-400B-8	Sequence 8, Appl
c 900	14	1.8	581	1	US-07-662-007B-36	Sequence 36, Appl	973	14	1.8	706	4	US-09-191-136-14	Sequence 14, Appl
c 901	14	1.8	581	1	US-07-824-247-36	Sequence 36, Appl	c 974	14	1.8	710	4	US-08-998-416-603	Sequence 603, App
c 902	14	1.8	581	3	US-08-470-204A-36	Sequence 36, Appl	c 975	14	1.8	715	4	US-08-901-789A-264	Sequence 264, App
c 903	14	1.8	581	4	US-09-385-982-12	Sequence 12, Appl	c 976	14	1.8	715	4	US-09-062-451-264	Sequence 264, App

Thu Oct 17 09:19:18 2002

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/679,451
FILING DATE: 19910402
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/179,100
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: GI 5180
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1607 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: homo sapiens
IMMEDIATE SOURCE:
CLONE: HUMBMPII-CDNA-39
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..355
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1544..1607
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 5,013,649
FILING DATE: 08-APR-1988
PUBLICATION DATE: 07-MAY-1991
US-07-679-451-1

Query Match 2.4%; Score 19; DB 1; Length 1607;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GCCCGAGGAGTGGAGGGC 281
|||||
DB 151 GCCCGAGGAGTGGAGGGC 133

RESULT 4
US-07-989-847-1/c
Sequence 1, Application US/07989847
Patent No. 5866364
GENERAL INFORMATION:
APPLICANT: Israel, David
TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140-2387
COMPUTER READABLE FORM:
MEDIUM TYPE: tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,847
FILING DATE:

CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI-5192B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 356..1543
US-07-989-847-1

Query Match 2.4%; Score 19; DB 2; Length 1607;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GCCCGAGGAGTGGAGGGC 281
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DB 151 GCCCGAGGAGTGGAGGGC 133

RESULT 5
US-07-721-847A-3/c
Sequence 3, Application US/07721847A
Patent No. 6150328
GENERAL INFORMATION:
APPLICANT: Wang, Elizabeth A.
APPLICANT: Rosen, Vicki A.
APPLICANT: Wozney, John M.
TITLE OF INVENTION: No. 6150328el BMP Products
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
STREET: 87 CAMBRIDGEPARK DRIVE
CITY: CAMBRIDGE
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/721,847A
FILING DATE: 14-JUN-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: 5160C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens

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; CELL TYPE: Osteosarcoma Cell Line
; CELL LINE: U-2OS
; IMMEDIATE SOURCE:
; LIBRARY: U2OS cDNA in Lambda GT10
; CLONE: Lambda U2OS-39
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1546
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1202..1543
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: 14..1607
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 356..424
; US-07-721-847A-3
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Best Local Similarity 100.0%; Pred. No. 5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GCCCGAGGAGTGGAGGGC 281
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DB 151 GCCCGAGGAGTGGAGGGC 133

RESULT 6
US-08-469-411-1/c
; Sequence 1, Application US/08469411
; Patent No. 6190880
; GENERAL INFORMATION:
; APPLICANT: Israel, David
; TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140-2387
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,411
; FILING DATE: 06-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI-5192B-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8622
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1543
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; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-469-411-1
Query Match 2.4%; Score 19; DB 4; Length 1607;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GCCCGAGGAGTGGAGGGC 281
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DB 151 GCCCGAGGAGTGGAGGGC 133

RESULT 7
US-08-925-779-3/C
; Sequence 3, Application US/08925779
; Patent No. 6245889
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wozney, John M.
; TITLE OF INVENTION: No. 6245889el BMP Products
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGEPARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,779
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/721,847
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: 5160C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; CELL TYPE: Osteosarcoma Cell Line
; CELL LINE: U-2OS
; IMMEDIATE SOURCE:
; LIBRARY: U2OS cDNA in Lambda GT10
; CLONE: Lambda U2OS-39
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 356..1546
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1202..1543
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; NAME/KEY: mRNA
; LOCATION: 14...1607
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 356...424
; US-08-925-779-3

Query Match      2.4%; Score 19; DB 4; Length 1607;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GCCCGAGGAGTGAGGGGC 281
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Db 151 GCCCGAGGAGTGAGGGGC 133

RESULT 8
5166058-3/c
; Patent No. 5166058
; APPLICANT: WANG, ELIZABETH A.; WOZNEY, JOHN M.; RPSN, VICKI A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING THE OSTEOINDUCTIVE
; PROTEINS
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/378,537
; FILING DATE: 11-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 179,100
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: 28,285
; FILING DATE: 20-MAR-1987
; APPLICATION NUMBER: 943,332
; FILING DATE: 17-DEC-1986
; APPLICATION NUMBER: 880,776
; FILING DATE: 01-JUL-1986
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; LENGTH: 1607
5166058-3

Query Match      2.4%; Score 19; DB 6; Length 1607;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GCCCGAGGAGTGAGGGGC 281
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Db 151 GCCCGAGGAGTGAGGGGC 133

RESULT 9
US-07-667-276A-3/c
; Sequence 3, Application US/07667276A
; Patent No. 5470971
; GENERAL INFORMATION:
; APPLICANT: Kondo, Keiji
; TITLE OF INVENTION: Inouye, Masayori
; TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
; THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
; TITLE OF INVENTION: APPLICATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 S. Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/667,276A
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; FILING DATE: 11-MAR-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 377,5351P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2017 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
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; ORGANISM: Saccharomyces cerevisiae
; STRAIN: S288C
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 484...1725
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Base #1 of Sequence No. 5470971 3
; OTHER INFORMATION: corresponds to base 483 of the sequence listed in
; OTHER INFORMATION: Figure 11 of the application"
US-07-667-276A-3

Query Match      2.4%; Score 19; DB 1; Length 2017;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
US-08-811-481-34
; Sequence 34, Application US/08811481
; Patent No. 6300093
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Jelinek, Laura J.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Hagopian, William A.
; APPLICANT: Lagasse, James W.
; TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,481
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
```

ATTORNEY/AGENT INFORMATION:
NAME: Lingenfelter, Susan
REGISTRATION NUMBER: P-41,156
REFERENCE/DOCKET NUMBER: 95-36
TELEPHONE: 206-442-6675
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 2328 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-811-481-34

Query Match 2.4%; Score 19; DB 4; Length 2328;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 763 TTCACCAAAAAAAAAAAAA 781
|||||
Db 2279 TTCACCAAAAAAAAAAAAA 2297

RESULT 11
US-08-377-687-48
; Sequence 48, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARB Y & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:

NAME/KEY: CDS
LOCATION: 16..255
US-08-377-687-48

Query Match 2.3%; Score 18; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 764 TTCACCAAAAAAAAAAAAA 781
|||||
Db 390 TTCACCAAAAAAAAAAAAA 407

RESULT 12
US-08-777-192-48
; Sequence 48, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARB Y & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
US-08-777-192-48

Query Match 2.3%; Score 18; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 764 TTCACCAAAAAAAAAAAAA 781
|||||
Db 390 TTCACCAAAAAAAAAAAAA 407


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: STREET: 755 PAGE MILL ROAD
: CITY: PALO ALTO
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/549,846
: FILING DATE: 01-NOV-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: DYLAN, TYLER
: REGISTRATION NUMBER: 37,612
: REFERENCE/DOCKET NUMBER: 22627-20013.01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 706141 MRSNFOERS SFO
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3585 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-08-549-846-2
:
: Query Match 2.3%; Score 18; DB 3; Length 3585;
: Best Local Similarity 100.0%; Pred. No. 15;
: Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 520 CAGCTGAGATCCCGATGCC 537
:
: Db 1977 CAGCTGAGATCCCGATGCC 1994
:
:
: RESULT 15
: PCT-US96-01314-39
: Sequence 39, Application PC/TUS9601314
: GENERAL INFORMATION:
: APPLICANT: M. Amin Arnaout
: TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
: TITLE OF INVENTION: ANTAGONISTS
: NUMBER OF SEQUENCES: 78
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: COMPUTER: IBM ps/2 Model 502 or 55SX
: OPERATING SYSTEM: MS-DOS (Version 5.0)
: SOFTWARE: WordPerfect (Version 5.1)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/01314
: FILING DATE: 30-JAN-96
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/380,167
: FILING DATE: 30-JAN-95
: ATTORNEY/AGENT INFORMATION:
: NAME: John W. Freeman
: REGISTRATION NUMBER: 29,066
: REFERENCE/DOCKET NUMBER: 00786/267001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-5070
: TELEFAX: (617) 542-8906
: TELEX: 200154

```

```

; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5137 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US96-01314-39

Query Match          2.3%; Score 18; DB 5; Length 5137;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 520 CAGCTGAGATCCCAAGTC 537
    |||||
Db 1971 CAGCTGAGATCCCAAGTC 1988

RESULT 17
US-08-611-280-4
; Sequence 4, Application US/08611280
; Patent No. 5891666
; GENERAL INFORMATION:
; APPLICANT: Matsuyama, Toshifumi
; APPLICANT: Grossman, Alex
; APPLICANT: Richardson, Christopher D.
; TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Canada Inc.
; STREET: 6733 Mississauga Road, Suite 303
; CITY: Mississauga
; STATE: Ontario
; COUNTRY: Canada
; ZIP: L5N 6J8
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611,280
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oleski, Nancy A.
; REGISTRATION NUMBER: 34,688
; REFERENCE/DOCKET NUMBER: A-338A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12537 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-611-280-4

Query Match          2.3%; Score 18; DB 2; Length 12537;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 492 GGCAGCAGACAGAGAA 509
    |||||
Db 4358 GGCAGCAGACAGAGAA 4375

RESULT 18
US-09-195-940-4
; Sequence 4, Application US/09195940
; Patent No. 6258935
; GENERAL INFORMATION:
; APPLICANT: Matsuyama, Toshifumi
; APPLICANT: Grossman, Alex
; APPLICANT: Richardson, Christopher D.
; TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Canada Inc.
; STREET: 6733 Mississauga Road, Suite 303
; CITY: Mississauga
; STATE: Ontario
; COUNTRY: Canada
; ZIP: L5N 6J8
; COMPUTER READABLE FORM:

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;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/195,940
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/611,280
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Oleski, Nancy A.
; REGISTRATION NUMBER: 34,688
; REFERENCE/DOCKET NUMBER: A-338A
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12537 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-195-940-4
;
Query Match 2.3%; Score 18; DB 4; Length 12537;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 492 GGGCAGCAGACAGAGAA 509
|||||
DB 4358 GGCAGCAGACAGAGAA 4375
;
RESULT 19
US-08-955-937A-3
; Sequence 3, Application US/08955937A
; Patent No. 6020161
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN
; TITLE OF INVENTION: GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,937A
; FILING DATE: 17-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,152
; FILING DATE: 19-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 708 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-955-937A-3
;
Query Match 2.2%; Score 17; DB 3; Length 708;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 273 TGGAGGGGCTCAGGCGA 289
|||||
DB 382 TGGAGGGGCTCAGGCGA 398
;
RESULT 20
US-09-300-985-3
; Sequence 3, Application US/09300985A
; Patent No. 6232441
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEMSEGED
; APPLICANT: HURLE, MARK ROBERT
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN GENE
; TITLE OF INVENTION: SUPERFAMILY
; FILE REFERENCE: GH-70228-1
; CURRENT APPLICATION NUMBER: US/09/300,985A
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US 08/955,937
; EARLIER FILING DATE: 1997-10-22
; EARLIER APPLICATION NUMBER: US 60/056,152
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 708
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (475)(620)(660)
; US-09-300-985-3
;
Query Match 2.2%; Score 17; DB 4; Length 708;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 273 TGGAGGGGCTCAGGCGA 289
|||||
DB 382 TGGAGGGGCTCAGGCGA 398
;
RESULT 21
US-08-123-161A-11
; Sequence 11, Application US/08123161A
; Patent No. 5449616
; GENERAL INFORMATION:
; APPLICANT: Campbell, Kevin P.
; APPLICANT: Roberts, Steven L.
; APPLICANT: Anderson, Richard D.
; APPLICANT: Ibraghimov, Oxana B.
; APPLICANT: Yang, Bin
; TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA

```
;
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,161A
; FILING DATE: 16-SEP-93
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/946,234
; FILING DATE: 14-SEP-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1396 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4..1164
; US-08-123-161A-11

Query Match 2.2%; Score 17; DB 1; Length 1396;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 TCACCAAAAAAAAAAAAA 781
Db 1366 TCACCAAAAAAAAAAAAA 1382

RESULT 22
US-08-483-278-11
; Sequence 11, Application US/08483278
; Patent No. 5686073
; GENERAL INFORMATION:
; APPLICANT: Campbell, Kevin P.
; APPLICANT: Ibraghimov, Oxana B.
; APPLICANT: Ervasti, James M.
; APPLICANT: Levellie, Cynthia J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,278
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,161
; FILING DATE: 16-SEP-93
; ATTORNEY/AGENT INFORMATION:
```

```
;
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: UIRF89-11A5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1396 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4..1164
; US-08-483-278-11

Query Match 2.2%; Score 17; DB 1; Length 1396;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 TCACCAAAAAAAAAAAAA 781
Db 1366 TCACCAAAAAAAAAAAAA 1382

RESULT 23
US-09-189-760-5
; Sequence 5, Application US/09189760
; Patent No. 6031078
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-046CP2
; CURRENT APPLICATION NUMBER: US/09/189,760
; CURRENT FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/163,116
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 60/089,467
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: (PENDING)
; EARLIER FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1529
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(749)
; US-09-189-760-5

Query Match 2.2%; Score 17; DB 3; Length 1529;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 TCACCAAAAAAAAAAAAA 781
Db 1420 TCACCAAAAAAAAAAAAA 1436

RESULT 24
US-09-188-811-5
; Sequence 5, Application US/09188811
; Patent No. 6037148
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MNI-046CP
```

Thu Oct 17 09:19:18 2002

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;
; CURRENT APPLICATION NUMBER: US/09/188,811
; CURRENT FILING DATE: 1998-11-09
; EARLIER APPLICATION NUMBER: 09/163,116
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1529
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(749)
US-09-188-811-5

Query Match      2.2%; Score 17; DB 3; Length 1529;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 TCACCAAAAAAAAAAAAA 781
Db 1420 TCACCAAAAAAAAAAAAA 1436

RESULT 25
US-09-514-422-5
; Sequence 5, Application US/09514422
; Patent No. 6291193
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-046CP2
; CURRENT APPLICATION NUMBER: US/09/514,422
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US/09/189,760
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/163,116
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/089,467
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: (PENDING)
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1529
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(749)
US-09-514-422-5

Query Match      2.2%; Score 17; DB 4; Length 1529;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 TCACCAAAAAAAAAAAAA 781
Db 1420 TCACCAAAAAAAAAAAAA 1436

RESULT 26
US-08-749-289-2/c
; Sequence 2, Application US/08749289
; Patent No. 5955301
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; TITLE OF INVENTION: NOVEL HUMAN GLUTAMATE-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 3
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,289
; FILING DATE: Filed Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0160 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1770 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 385116
US-08-749-289-2

Query Match      2.2%; Score 17; DB 2; Length 1770;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 655 GAACGAGTGAAGAGCA 671
Db 1029 GAACGAGTGAAGAGCA 1013

RESULT 27
US-08-878-563A-2
; Sequence 2, Application US/08878563A
; Patent No. 5891674
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: INSULIN RECEPTOR TYROSINE KINASE SUBSTRATE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,563A
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
```

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0323 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2080 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT04
; CLONE: 918158
;
US-08-878-563A-2
;
Query Match 2.2%; Score 17; DB 2; Length 2080;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 GTCCACAGGCAGATCCA 93
Db 339 GTCCACAGGCAGATCCA 355

RESULT 28
US-09-270-117-2
; Sequence 2, Application US/09270117
; Patent No. 6265550
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: INSULIN RECEPTOR TYROSINE KINASE SUBSTRATE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
;
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,117
FILING DATE:
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 08/878,563
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0323 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2080 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRSTNOT04
CLONE: 918158
;
US-09-270-117-2

```

```

Query Match 2.2%; Score 17; DB 4; Length 2080;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 GTCCACAGGCAGATCCA 93
Db 339 GTCCACAGGCAGATCCA 355

RESULT 29
US-08-955-937A-1
; Sequence 1, Application US/08955937A
; Patent No. 6020161
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN
; TITLE OF INVENTION: GENE SUPERFAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
;
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,937A
FILING DATE: 17-OCT-1997
PRIOR APPLICATION DATA:
CLASSIFICATION: 435
APPLICATION NUMBER: 60/056,152
FILING DATE: 19-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-955-937A-1

Query Match 2.2%; Score 17; DB 3; Length 2345;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 TGGAGGGGCTCAGGCGA 289
Db 403 TGGAGGGGCTCAGGCGA 419

RESULT 30
US-09-300-985-1
; Sequence 1, Application US/09300985A
; Patent No. 6232441
; GENERAL INFORMATION:
; APPLICANT: WU, SHUJIAN
; APPLICANT: SWEET, RAYMOND W.

```

```

; APPLICANT: TRUNEH, ALEMSEGED
; APPLICANT: HURLE, MARK ROBERT
; TITLE OF INVENTION: PIGR-1, A MEMBER OF IMMUNOGLOBULIN GENE
; TITLE OF INVENTION: SUPERFAMILY
; FILE REFERENCE: GH-70228-1
; CURRENT APPLICATION NUMBER: US/09/300,985A
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US 08/955,937
; EARLIER FILING DATE: 1997-10-22
; EARLIER APPLICATION NUMBER: US 60/056,152
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2345
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; US-09-300-985-1

Query Match      2.2%; Score 17; DB 4; Length 2345;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 TGGAGGGGCTCAGCGCA 289
|||||
Db 403 TGGAGGGGCTCAGCGCA 419

RESULT 31
US-09-189-760-1
; Sequence 1, Application US/09189760
; Patent No. 6031078
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-046CP2
; CURRENT APPLICATION NUMBER: US/09/189,760
; CURRENT FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/163,116
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 60/089,467
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: (PENDING)
; EARLIER FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (164)..(1714)
; US-09-189-760-1

Query Match      2.2%; Score 17; DB 3; Length 2494;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 765 TCACCAAAAAAAAAAAAA 781
|||||
Db 2385 TCACCAAAAAAAAAAAAA 2401

RESULT 32
US-09-514-422-1
; Sequence 1, Application US/09514422
; Patent No. 6291193
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-046CP2
; CURRENT APPLICATION NUMBER: US/09/514,422
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US/09/189,760
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/163,116
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/089,467
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: (PENDING)
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (164)..(1714)
; US-09-514-422-1

Query Match      2.2%; Score 17; DB 4; Length 2494;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 765 TCACCAAAAAAAAAAAAA 781
|||||
Db 2385 TCACCAAAAAAAAAAAAA 2401

RESULT 33
US-08-162-081B-35
; Sequence 35, Application US/08162081B
; Patent No. 5824492
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,081B
; FILING DATE: February 7, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: nucleic acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-162-081B-35

Query Match          2.2%  Score 17; DB 1; Length 3207;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 629 CTAAGAGGAACTGT 645
Db 1244 CTAAGAGGAACTGT 1260
|||||

RESULT 34
US-08-780-872-35
; Sequence 35, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,957
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/780,872
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-085-957-35

Query Match          2.2%  Score 17; DB 4; Length 3207;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 629 CTAAGAGGAACTGT 645
Db 1244 CTAAGAGGAACTGT 1260
|||||

RESULT 36
US-08-162-081B-34
; Sequence 34, Application US/08162081B
; Patent No. 5824492
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
```



```

; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,081B
; FILING DATE: February 7, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-162-081B-34

```

Query Match 2.2%; Score 17; DB 1; Length 3240;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 629 CTAAGAGGACACTGT 645
DB 1244 CTAAGAGGACACTGT 1260

```

RESULT 37

```

; US-08-780-872-34
; Sequence 34, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.

```

```

; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-780-872-34

```

Query Match 2.2%; Score 17; DB 2; Length 3240;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 629 CTAAGAGGACACTGT 645
DB 1244 CTAAGAGGACACTGT 1260

```

RESULT 38

```

; US-09-085-957-34
; Sequence 34, Application US/09085957
; Patent No. 6274327
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,957
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/780,872
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-085-957-34

```

Query Match 2.2%; Score 17; DB 4; Length 3240;

```
Best Local Similarity 100.0%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 629 CTAAGAGGAACACTGT 645
| | | | | | | | | | | | | | | | | |
Db 1244 CTAAGAGGAACACTGT 1260

RESULT 39
US-08-162-081B-32
; Sequence 32, Application US/08162081B
; Patent No. 5824492
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala: Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefan; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3412 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single or double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3204
; OTHER INFORMATION: /standard_name= "CDS"
US-08-162-081B-32

Query Match 2.2%; Score 17; DB 1; Length 3412;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 629 CTAAGAGGAACACTGT 645
| | | | | | | | | | | | | | | | | |
Db 1244 CTAAGAGGAACACTGT 1260

Search completed: October 16, 2002, 23:02:33
Job time : 94 secs
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OM nucleic - nucleic search, using sw model

Run on: October 16, 2002, 21:07:21 ; Search time 1610 Seconds
(without alignments)
6547 281 Million cell updates/sec

Title: US-09-658-824-808
Perfect score: 781
Sequence: 1 ggcgcggaagctatgtgcccg.....ctttcccaaaaaaaaaaaa 781

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 10
Total number of hits satisfying chosen parameters: 10313871

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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post-processing: Listing first 1000 summaries

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Database : EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_gss.*
13: em_gss_hum.*
14: em_gss_inv.*
15: em_gss_pln.*
16: em_gss_vrt.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	521	66.7	785	10	BE875341	BE875341	601489051
2	489	62.6	489	10	BE81023	BE81023	601490780
3	390	49.9	486	10	B1460303	B1460303	603201939
4	390	49.9	487	10	BE772292	BE772292	602722580
5	390	49.9	880	10	BE876234	BE876234	601486758
C 6	379	48.5	428	9	AA948244	AA948244	0Q33g01.s
	378	48.4	414	9	AA620697	AA620697	af89d01.s
C 8	367	47.0	438	9	A1954712	A1954712	wq32c10..x
C 9	360	46.1	1140	10	BE620196	BE620196	601483262
C 10	359	46.0	421	9	A1631681	A1631681	wb08d02..x
C 11	338	43.3	556	9	AW975988	AW975988	EST388097
C 12	335	42.9	423	9	AA648117	AA648117	ns06d07..r
C 13	310	39.7	407	9	AA758618	AA758618	ah58d07..s
C 14	288	36.9	485	10	BG217244	BG217244	RST36946
C 15	281	36.0	665	9	AV682444	AV682444	AV682444
C 16	274	35.1	384	10	BG216048	BG216048	RST35862
C 17	259	33.2	398	10	BC206865	BC206865	RST26327

91	21	2.7	498	10	BF045827	BF045827 BP250005A	c 164	19	2.4	251	9	AI808093	AI808093.at19f03.x
c 92	21	2.7	500	9	AI402186	AI402186 GH09786.3	c 165	19	2.4	254	10	BI428179	BI428179.f175608.x
93	21	2.7	525	10	BM419880	BM419880 R02D0B0.0	c 166	19	2.4	257	10	BG220980	BG220980.RST40780
94	21	2.7	547	10	BE681607	BE681607 179329 MA	c 167	19	2.4	257	10	BG579452	BG579452.dab75b05.
c 95	21	2.7	564	12	BH616877	BH616877 BMBAC310H	c 168	19	2.4	261	10	BF466628	BF466628.U1-M-CG0p
c 96	21	2.7	886	10	BI695973	BI695973 603346165	c 169	19	2.4	262	9	AW066672	AW066672.683006A02
c 97	21	2.7	923	12	CNS003XB	AL065285 Drosophil	c 170	19	2.4	262	10	BM334876	BM334876.MEST143-C
c 98	21	2.7	1527	12	AG135591	AG135591 Pan trogl	c 171	19	2.4	262	10	BE995399	BE995399.U1-M-CG0p
c 99	20	2.6	240	9	BF470674	BF470674 UI-M-BH3-	c 172	19	2.4	275	9	AV742275	AV742275.AV742275
c 100	20	2.6	240	9	AI556212	AI556212 UI-R-C2p-	c 173	19	2.4	276	12	AQ108362	AQ108362.CIT-HSP-2
c 101	20	2.6	277	10	BE949311	BE949311 UI-M-BH3-	c 174	19	2.4	284	9	AU031091	AU031091.AU031091
c 102	20	2.6	292	10	BE990047	BE990047 UI-M-B21-	c 175	19	2.4	287	9	AU031091	AU031091.AU031091
c 103	20	2.6	312	10	BF408985	BF408985 UI-R-BJ2-	c 176	19	2.4	285	9	BB420880	BB420880.BB420880
c 104	20	2.6	343	9	AW204002	AW204002 UI-H-B11-	c 177	19	2.4	287	10	BF711597	BF711597.M1-P-A1-a
c 105	20	2.6	343	10	BF398312	BF398312 UI-R-B52-	c 178	19	2.4	289	9	BB251667	BB251667.BB251667
c 106	20	2.6	351	10	BE525130	BE525130 M58H1STM	c 179	19	2.4	293	9	BB009833	BB009833.BB009833
c 107	20	2.6	367	10	BE955270	BE955270 UI-M-CG0p	c 180	19	2.4	298	9	AW655358	AW655358.105984 MA
c 108	20	2.6	379	10	D55484	D55484 HUM180B09B	c 181	19	2.4	308	9	AW523054	AW523054.U1-R-B00-
c 109	20	2.6	386	9	AA817964	AA817964 UI-R-A0-a	c 182	19	2.4	308	10	BG555746	BG555746.df20h05.x
c 110	20	2.6	398	9	AI715284	AI715284 UI-R-Y0-a	c 183	19	2.4	313	9	BB396707	BB396707.BB396707
c 111	20	2.6	442	9	AU172665	AU172665 AU172665	c 184	19	2.4	316	9	BB451464	BB451464.BB451464
c 112	20	2.6	456	9	AV739448	AV739448 AV739448	c 185	19	2.4	318	9	AW073875	AW073875.xb04C10.x
c 113	20	2.6	465	9	BB855812	BB855812 BB855812	c 186	19	2.4	323	10	BM372304	BM372304.EBr003_SQ
c 114	20	2.6	466	12	AZ294141	AZ294141 RPCT-23-1	c 187	19	2.4	325	10	AI510997	AI510997.U1-R-C2p-
c 115	20	2.6	474	9	AW159644	AW159644 zb05b07.x	c 188	19	2.4	325	10	BM337332	BM337332.MBST149-C
c 116	20	2.6	479	9	AW400088	AW400088 707051B11	c 189	19	2.4	326	9	AA179328	AA179328.zp12b02.r
c 117	20	2.6	479	9	AW452932	AW452932 UI-H-BW1-	c 190	19	2.4	327	4	BB070581	BB070581.Mus_muscu
c 118	20	2.6	510	10	BI400173	BI400173 M1-P-A11-	c 191	19	2.4	334	10	BI491308	BI491308.df06h11.w
c 119	20	2.6	519	10	BM266318	BM266318 VL83 cdNA	c 192	19	2.4	343	9	AA497170	AA497170.f01908.s
c 120	20	2.6	548	9	BE113957	BE113957 UI-R-BJ1-	c 193	19	2.4	348	10	BI000385	BI000385.MR3-HN006
c 121	20	2.6	570	12	AZ467193	AZ467193 1M0278J20	c 194	19	2.4	349	9	AI304085	AI304085.EST00090
c 122	20	2.6	576	12	CNS037VM	AL260347 Tetraodon	c 195	19	2.4	349	9	BE138496	BE138496.x176a10.x
c 123	20	2.6	605	12	AQ959104	AQ959104 LERPH33TF	c 196	19	2.4	350	10	BF273284	BF273284.GA_Eb001
c 124	20	2.6	613	12	AZ821669	AZ821669 2M0094102	c 197	19	2.4	351	9	AI544994	AI544994.f073d03.x
c 125	20	2.6	646	10	BG841415	BG841415 MEST21-D0	c 198	19	2.4	356	9	AU101146	AU101146.AU101146
c 126	20	2.6	670	12	CNS02P51	AL194590 Tetraodon	c 199	19	2.4	356	10	BI493375	BI493375.d1010c06..
c 127	20	2.6	693	12	AZ461440	AZ461440 1M0267L15	c 200	19	2.4	360	9	AI029102	AI029102.U1-R-C0-1
c 128	20	2.6	714	12	AQ959105	AQ959105 LERPH33TF	c 201	19	2.4	360	10	C40203	C40203.C40203.YuJ1
c 129	20	2.6	776	12	BH054219	BH054219 RPCT-24-3	c 202	19	2.4	363	9	AI396151	AI396151.487012A09
c 130	20	2.6	836	10	BI102740	BI102740 602888317	c 203	19	2.4	363	9	AI396189	AI396189.487012F08
c 131	20	2.6	884	10	BF573878	BF573878 602132085	c 204	19	2.4	365	9	AI396159	AI396159.487012B08
c 132	20	2.6	898	12	CNS0123J	AL101065 Drosophil	c 205	19	2.4	366	10	BF597638	BF597638.su87d008.y
c 133	20	2.6	992	10	BG391711	BG391711 602417991	c 206	19	2.4	368	10	BG294675	BG294675.602392041
c 134	20	2.6	1019	12	CNS03XK5	AL265370 Tetraodon	c 207	19	2.4	368	10	BI806960	BI806960.S080810.S
c 135	20	2.6	1135	12	AG126408	AG126408 Pan trogl	c 208	19	2.4	369	9	AA271000	AA271000.va85d07.r
c 136	20	2.6	2087	11	BC010625	BC010625 Homo sapi	c 209	19	2.4	371	9	AA937811	AA937811.nw89b06.s
c 137	19	2.4	101	9	BE043556	BE043556 hk40b05.Y	c 210	19	2.4	371	9	AI395271	AI395271.MA002782
c 138	19	2.4	127	9	AW881391	AW881391 OV4-OT003	c 211	19	2.4	372	10	BI900766	BI900766.lb81a08.y
c 139	19	2.4	138	10	BE663162	BE663162 133617.MA	c 212	19	2.4	374	10	F36051	F36051.HSPD33359.H
c 140	19	2.4	150	9	AI940262	AI940262 CM3-CT003	c 213	19	2.4	378	9	AI974482	AI974482.T110432e
c 141	19	2.4	160	9	BE111941	BE111941 UI-R-B51-	c 214	19	2.4	378	12	AQ731336	AQ731336.HS_5512.B
c 142	19	2.4	168	10	N57994	N57994.YV62F07.s1	c 215	19	2.4	385	9	BE104509	BE104509.U1-R-BX0-
c 143	19	2.4	169	9	AI934411	AI934411 wp05d12.x	c 216	19	2.4	387	10	BG441767	BG441767.GA_Ea001
c 144	19	2.4	169	10	BI934411	BI934411 wp05d12.x	c 217	19	2.4	388	10	BM358944	BM358944.GA_Ea001
c 145	19	2.4	174	9	AV140319	AV140319 AV140319	c 218	19	2.4	388	12	AQ526468	AQ526468.HS_5309.B
c 146	19	2.4	176	9	AI828599	AI828599.w142904.x	c 219	19	2.4	391	9	BE103967	BE103967.U1-R-BX0-
c 147	19	2.4	180	10	BF713062	BF713062.M1-P-H3-a	c 220	19	2.4	396	10	BE195195	BE195195.RST14374
c 148	19	2.4	189	10	BI294600	BI294600.U1-R-DK0-	c 221	19	2.4	397	9	AA086008	AA086008.zn64h03.r
c 149	19	2.4	190	10	BI805139	BI805139.S005E11.S	c 222	19	2.4	398	9	AI396158	AI396158.487012B07
c 150	19	2.4	191	9	AU071425	AU071425 AU071425	c 223	19	2.4	399	10	BG195736	BG195736.RST14930
c 151	19	2.4	209	9	AW834597	AW834597.MR2-TT001	c 224	19	2.4	400	10	BG994061	BG994061.PM0-HT091
c 152	19	2.4	209	9	BE149111	BE149111.RC4-HT025	c 225	19	2.4	402	10	BM075692	BM075692.MEST359-B
c 153	19	2.4	215	9	AI585048	AI585048.f669g06.x	c 226	19	2.4	404	9	AI582900	AI582900.t507d04.x
c 154	19	2.4	220	10	BF820389	BF820389.MR1-RT004	c 227	19	2.4	404	9	AV706881	AV706881.AV706881
c 155	19	2.4	221	9	AI563608	AI563608.vx91f04.x	c 228	19	2.4	405	10	BG895250	BG895250.358571.MA
c 156	19	2.4	228	10	BG272561	BG272561.nah34908.	c 229	19	2.4	407	9	AI454462	AI454462.U1-R-C2p-
c 157	19	2.4	229	9	AW600647	AW600647 707104E02	c 230	19	2.4	411	9	AU183353	AU183353.AU183353
c 158	19	2.4	236	9	BB048238	BB048238.BB048238	c 231	19	2.4	412	9	BE232382	BE232382.137390.MA
c 159	19	2.4	239	9	AI917241	AI917241.t553d09.x	c 232	19	2.4	413	10	BE984741	BE984741.U1-M-CG0p
c 160	19	2.4	240	9	AU071424	AU071424 AU071424	c 233	19	2.4	413	10	BE984744	BE984744.U1-M-CG0p
c 161	19	2.4	242	10	BI004685	BI004685.CM0-HN020	c 234	19	2.4	416	12	AZ135172	AZ135172.OSJRB011
c 162	19	2.4	248	9	BE216655	BE216655.hv_Ceb001	c 235	19	2.4	417	10	BI290953	BI290953.U1-R-DK0-
c 163	19	2.4	249	9	AI588892	AI588892.tq28h09.x	c 236	19	2.4	418	9	AA252078	AA252078.z163f04.s

c 237	19	2.4	420	10	B8811889	B8811889 PM0-AN003	310	19	2.4	541	12	AZ738381	AZ738381 RPC1-24-1
c 238	19	2.4	421	12	A0277358	A0277358 C1B1-E1-	c 311	19	2.4	544	9	AN049843	AN049843 UI-M-BH1-
c 239	19	2.4	422	10	A1662312	A1662312 ms08c10.x	312	19	2.4	544	10	BG756327	BG756327 602713646
c 240	19	2.4	423	9	BB699421	BB699421 BB699421	313	19	2.4	544	10	B1795438	B1795438 6021f06 E
c 241	19	2.4	426	10	BF516028	BF516028 UI-H-BW1-	314	19	2.4	546	10	BG763052	BG763052 602734931
c 242	19	2.4	427	9	AW562844	AW562844 660067F01	315	19	2.4	546	10	BG769167	BG769167 602743251
c 243	19	2.4	431	9	AI442274	AI442274 sa26c11.x	316	19	2.4	547	9	BE234412	BE234412 141414 MA
c 244	19	2.4	431	9	AI713902	AI713902 UI-R-AC1-	c 317	19	2.4	547	10	BM332924	BM332924 MEST181-E
c 245	19	2.4	435	9	AA118985	AA118985 mp64005.f	c 318	19	2.4	548	10	BM266863	BM266863 MEST387-P
c 246	19	2.4	435	9	AW135797	AW135797 UI-H-B11-	c 319	19	2.4	548	12	AZ969771	AZ969771 2M024210f
c 247	19	2.4	435	10	BE848045	BE848045 uw32b06.y	320	19	2.4	549	10	BG684619	BG684619 602636393
c 248	19	2.4	438	9	AW973753	AW973753 EST385854	c 321	19	2.4	551	10	BM268493	BM268493 MEST396-D
c 249	19	2.4	443	10	BM333167	BM333167 MEST184-H	322	19	2.4	551	12	AZ394429	AZ394429 1M0158E01
c 250	19	2.4	448	9	AU090156	AU090156 AU090156	323	19	2.4	554	10	B1860057	B1860057 603387235
c 251	19	2.4	450	12	AQ144755	AQ144755 HS_3092_A	c 324	19	2.4	556	10	BG194648	BG194648 RST13812
c 252	19	2.4	451	9	AV618633	AV618633 AV618633	325	19	2.4	558	10	EG204372	EG204372 RST23774
c 253	19	2.4	458	10	BF410519	BF410519 UI-R-CA0-	326	19	2.4	558	10	BM421785	BM421785 V019G10 O
c 254	19	2.4	459	9	BB863368	BB863368 BB863368	327	19	2.4	559	9	AV738206	AV738206 AV738206
c 255	19	2.4	462	9	BE111663	BE111663 UI-R-BJ1-	328	19	2.4	559	10	BE500751	BE500751 MHE0991-O
c 256	19	2.4	464	10	BE853234	BE853234 uw86d09.x	329	19	2.4	561	10	BE410489	BE410489 601301913
c 257	19	2.4	466	9	AW161946	AW161946 au71h09.x	c 330	19	2.4	562	9	AW180963	AW180963 MqA0095f
c 258	19	2.4	468	10	BM338233	BM338233 MEST2223-F	c 331	19	2.4	567	10	BG266572	BG266572 1000097D1
c 259	19	2.4	468	10	BM331984	BM331984 MEST173-E	c 332	19	2.4	567	10	BM351647	BM351647 MEST344-C
c 260	19	2.4	469	12	AQ607665	AQ607665 HS_5408_A	c 333	19	2.4	569	10	BG266572	BG266572 MEST344-C
c 261	19	2.4	471	12	AQ887433	AQ887433 HS_5555_A	c 334	19	2.4	569	12	AZ477423	AZ477423 1M0296H23
c 262	19	2.4	478	9	AI560424	AI560424 tn09h12.x	c 335	19	2.4	571	9	B8652116	B8652116 BB652116
c 263	19	2.4	478	9	AL385706	AL385706 MLCBC30B05	c 336	19	2.4	574	9	AI834591	AI834591 606070D09
c 264	19	2.4	479	10	BG375691	BG375691 UI-R-CS0-	c 337	19	2.4	575	10	B1865772	B1865772 ft26h07.x
c 265	19	2.4	479	10	BI7272150	BI7272150 NF021C11F	c 338	19	2.4	575	10	BE853468	BE853468 uw32b06.x
c 266	19	2.4	480	9	AW503991	AW503991 UI-HF-BN0	c 339	19	2.4	585	10	BM421924	BM421924 V021H11 O
c 267	19	2.4	480	9	BB635613	BB635613 BB635613	c 340	19	2.4	587	9	AW700855	AW700855 p845a02.y
c 268	19	2.4	481	9	AU095220	AU095220 AU095220	c 342	19	2.4	593	9	AV760729	AV760729 AV760729
c 269	19	2.4	481	10	BI495116	BI495116 df115b09.	c 343	19	2.4	593	10	BJ025715	BJ025715 BJO25715
c 270	19	2.4	486	9	AA075354	AA075354 zm87q07.s	c 344	19	2.4	593	12	AZ744550	AZ744550 RPC1-24-1
c 271	19	2.4	486	10	BI788550	BI788550 ie40e07.x	c 345	19	2.4	593	12	AQ381037	AQ381037 RPC111-13
c 272	19	2.4	487	9	AW531279	AW531279 UI-R-RS0-	c 346	19	2.4	597	10	BM266342	BM266342 MEST380-B
c 273	19	2.4	488	10	BM419343	BM419343 R012E11 O	c 347	19	2.4	597	12	AQ381081	AQ381081 RPC111-13
c 274	19	2.4	490	10	BE333018	BE333018 us97d06.y	c 348	19	2.4	598	10	BM333589	BM333589 MEST158-A
c 275	19	2.4	491	9	AA806538	AA806538 OC24B02.s	c 349	19	2.4	610	10	BG268727	BG268727 MEST399-D
c 276	19	2.4	491	9	AA526015	AA526015 n158d06.s	c 350	19	2.4	610	12	AZ763823	AZ763823 1M0559023
c 277	19	2.4	492	9	AA530910	AA530910 n197f11.s	c 351	19	2.4	615	10	BG344727	BG344727 HVSMEG001
c 278	19	2.4	492	10	BF278981	BF278981 GA_Eb003	c 352	19	2.4	617	10	BM3337601	BM3337601 MEST209-A
c 279	19	2.4	494	10	BF350609	BF350609 PM1-HT034	c 353	19	2.4	617	12	AQ365641	AQ365641 nbxb00640
c 280	19	2.4	498	10	BM351415	BM351415 MEST341-B	c 354	19	2.4	617	12	AQ365641	AQ365641 nbxb00640
c 281	19	2.4	503	10	BM332858	BM332858 MEST180-E	c 355	19	2.4	621	9	AA968363	AA968363 uc71f02.x
c 282	19	2.4	503	10	BF177687	BF177687 Ljirnpst	c 356	19	2.4	626	9	AA968363	AA968363 uc71f02.x
c 283	19	2.4	509	9	AI137144	AI137144 UI-R-C2p-	c 357	19	2.4	630	10	BM267162	BM267162 MEST391-A
c 284	19	2.4	509	9	AW424169	AW424169 sh61g12.y	c 358	19	2.4	631	9	AL638174	AL638174 AL638174
c 285	19	2.4	510	10	BG397853	BG397853 602438947	c 359	19	2.4	632	10	BM335113	BM335113 MEST145-G
c 286	19	2.4	511	10	BF976030	BF976030 602244856	c 360	19	2.4	634	9	BB654539	BB654539 BB654539
c 287	19	2.4	511	10	BG341679	BG341679 602463402	c 361	19	2.4	636	9	AI055456	AI055456 coau000A
c 288	19	2.4	513	10	N98756	N98756 zb85a06.s1	c 362	19	2.4	637	10	BM3339332	BM3339332 MEST240-A
c 289	19	2.4	514	9	AW185477	AW185477 se79a05.y	c 363	19	2.4	641	9	AW666939	AW666939 GA_Ea000
c 290	19	2.4	514	10	BI491296	BI491296 df06g02.w	c 364	19	2.4	642	12	BH123201	BH123201 RPC1-24-2
c 291	19	2.4	514	10	BM333138	BM333138 MEST184-E	c 365	19	2.4	646	9	BB391961	BB391961 BB391961
c 292	19	2.4	515	9	BB701448	BB701448 BB701448	c 366	19	2.4	648	9	BB609370	BB609370 BB609370
c 293	19	2.4	516	10	BM421645	BM421645 V017G01 O	c 367	19	2.4	652	10	BM269225	BM269225 MEST406-F
c 294	19	2.4	516	10	BF551324	BF551324 UI-R-C0-1	c 368	19	2.4	653	12	BH124979	BH124979 RPC1-24-3
c 295	19	2.4	519	10	BG811700	BG811700 daf35e07.	c 369	19	2.4	654	12	AQ874250	AQ874250 UI05D6.mt
c 296	19	2.4	523	10	BI879984	BI879984 fm68c03.x	c 370	19	2.4	658	10	BE907319	BE907319 601500028
c 297	19	2.4	524	12	AZ992161	AZ992161 2M0276007	c 371	19	2.4	660	10	BJ011463	BJ011463 BJ011463
c 298	19	2.4	525	12	AZ648929	AZ648929 1M0518H02	c 372	19	2.4	664	10	BG097566	BG097566 ES7462085
c 299	19	2.4	526	10	BG323192	BG323192 602421402	c 373	19	2.4	666	9	BB622597	BB622597 BB622597
c 300	19	2.4	527	10	BI813671	BI813671 M002D02 O	c 374	19	2.4	668	12	AQ548213	AQ548213 RPC1-11-4
c 301	19	2.4	527	10	BM333306	BM333306 MEST188-H	c 375	19	2.4	669	12	AZ574127	AZ574127 323PvB07
c 302	19	2.4	531	10	BM334919	BM334919 MEST130-A	c 376	19	2.4	672	10	BF786886	BF786886 602108815
c 303	19	2.4	531	10	BF515156	BF515156 UI-H-BW1-	c 377	19	2.4	673	12	AZ880966	AZ880966 RPC1-23-2
c 304	19	2.4	532	9	AI752264	AI752264 cn14f05.y	c 378	19	2.4	676	10	BG452759	BG452759 NF081B04L
c 305	19	2.4	532	12	TA314F09Q	TA314F09Q T_brucet	c 379	19	2.4	677	10	BI110864	BI110864 602895521
c 306	19	2.4	536	12	AZ128698	AZ128698 OSJNB009	c 380	19	2.4	677	12	AG114870	AG114870 Pan troq1
c 307	19	2.4	538	10	BM012778	BM012778 603637493	c 381	19	2.4	678	9	AV233538	AV233538 AV233538
c 308	19	2.4	538	10	BE519235	BE519235 946094G11	c 382	19	2.4	679	9	BB621608	BB621608 BB621608

383	19	2.4	680	9	BB496196	BB496196	456	18	2.3	146	9	AW102423	AW102423	s887905.y
c 384	19	2.4	681	10	BM268293	MEST379-C	c 457	18	2.3	153	10	BF413865	BF413865	UT-R-CAO-
c 385	19	2.4	681	12	BH546884	BOCHR46TR	c 458	18	2.3	156	10	BG796706	BG796706	UTSM-5M4C
c 386	19	2.4	682	10	BE457796	us97406.x	c 459	18	2.3	158	12	AQ202583	AQ202583	RPCI111-67
c 387	19	2.4	683	10	BM336552	MEST195-E	c 460	18	2.3	159	9	AU165237	AU165237	AU165237
c 388	19	2.4	686	10	BM074801	MEST297-G	c 461	18	2.3	164	10	BF632472	BF632472	NF040F04D
c 389	19	2.4	687	10	BM268287	MEST379-B	c 462	18	2.3	176	12	AQ900992	AQ900992	CSSTC0827
c 390	19	2.4	687	10	BM334548	MEST138-E	c 463	18	2.3	180	9	BE007892	BE007892	QVO-BN014
c 391	19	2.4	689	10	B1335227	602998123	c 464	18	2.3	185	9	BB321552	BB321552	PA09F02.y
c 392	19	2.4	694	12	AZ703477	RPCI-23-2	c 465	18	2.3	186	9	AW588233	AW588233	mh18b05.f
c 393	19	2.4	696	12	B67072	CJT-HSP-201	c 466	18	2.3	189	9	AA014745	AA014745	YU62C03.s1
c 394	19	2.4	697	12	AZ477093	IM0296H23	c 467	18	2.3	190	10	H64397	H64397	YU62C03.s1
c 395	19	2.4	699	10	BM337919	MEST219-B	c 468	18	2.3	193	9	AV026747	AV026747	AV026747
c 396	19	2.4	722	12	BH033898	RPCI-24-2	c 469	18	2.3	200	9	AI320464	AI320464	CSC05um.f
c 397	19	2.4	723	10	BM335663	MEST164-G	c 470	18	2.3	209	9	AV421167	AV421167	AV421167
c 398	19	2.4	724	10	BM339178	MEST237-F	c 471	18	2.3	215	9	AV224372	AV224372	AV224372
c 399	19	2.4	725	10	BM348599	MEST293-F	c 472	18	2.3	215	9	AA293052	AA293052	z154d04.f
c 400	19	2.4	727	10	BM332094	MEST152-C	c 473	18	2.3	215	10	D23188	D23188	RIC2396A.R
c 401	19	2.4	733	10	EG088921	H3159D02	c 474	18	2.3	216	9	AI311051	AI311051	t45905.x
c 402	19	2.4	738	10	EG206536	RST25987	c 475	18	2.3	216	9	AI311061	AI311061	t45H05.x
c 403	19	2.4	745	10	BM049709	603624216	c 476	18	2.3	216	9	AI335306	AI335306	t45H05.x
c 404	19	2.4	747	10	BM333846	MEST127-H	c 477	18	2.3	216	9	AV107276	AV107276	t45H05.x
c 405	19	2.4	754	10	BE255574	601111779	c 478	18	2.3	219	9	BB074037	BB074037	AV107276
c 406	19	2.4	768	10	BG077936	H3020F12-	c 479	18	2.3	220	9	AV163043	AV163043	BB074037
c 407	19	2.4	776	12	AZ133005	OSJNB010	c 480	18	2.3	222	10	BM187060	BM187060	AV163043
c 408	19	2.4	785	9	AI303541	u180q11.x	c 481	18	2.3	223	10	BM187060	BM187060	AV163043
c 409	19	2.4	789	10	BE368703	601222667	c 482	18	2.3	227	9	AI320188	AI320188	AGENCOURT
c 410	19	2.4	794	10	BE961893	601648321	c 483	18	2.3	229	10	BF780651	BF780651	FM181e07.y
c 411	19	2.4	798	12	BH352429	CH230-33D	c 484	18	2.3	230	10	BF780651	BF780651	FM181e07.y
c 412	19	2.4	800	10	BE783117	601470716	c 485	18	2.3	234	9	AA676080	AA676080	clh09nm.f
c 413	19	2.4	805	10	BG398667	602440274	c 486	18	2.3	234	9	AA676080	AA676080	bsf11nm.f
c 414	19	2.4	828	10	BG545588	602572843	c 487	18	2.3	235	12	AQ881790	AQ881790	TENF0608
c 415	19	2.4	830	10	BG755416	602713974	c 488	18	2.3	238	9	AV425036	AV425036	MRO-BT024
c 416	19	2.4	830	10	BE568447	601342532	c 489	18	2.3	238	12	BH509559	BH509559	HS-5267_A
c 417	19	2.4	847	10	EG180096	602329670	c 490	18	2.3	239	9	AV417837	AV417837	AV425036
c 418	19	2.4	848	12	CNS035A0	AL228489	c 491	18	2.3	239	9	AV417837	AV417837	BOHMM32TF
c 419	19	2.4	849	10	BF3250193	602362309	c 492	18	2.3	240	10	H64445	H64445	AV417837
c 420	19	2.4	853	10	BF342443	602013948	c 493	18	2.3	243	9	AV232664	AV232664	AV417837
c 421	19	2.4	858	10	BF123654	601760582	c 494	18	2.3	250	9	AV412809	AV412809	AV232664
c 422	19	2.4	860	12	AQ273862	nbxb0031D	c 495	18	2.3	254	9	AW100656	AW100656	AV412809
c 423	19	2.4	872	10	BI771964	603058994	c 496	18	2.3	254	9	BB280343	BB280343	AV412809
c 424	19	2.4	882	12	AZ207783	SP_0134_A	c 497	18	2.3	257	9	BB325964	BB325964	BB280343
c 425	19	2.4	896	10	BF698958	602126547	c 498	18	2.3	257	10	BI278065	BI278065	BB325964
c 426	19	2.4	898	9	BE052093	GA_Ea003	c 499	18	2.3	260	9	AI059224	AI059224	BI278065
c 427	19	2.4	908	10	BE244865	602358307	c 500	18	2.3	260	9	AI059224	AI059224	UI-R-C1-1
c 428	19	2.4	930	12	CNS01S3C	AL164721	c 501	18	2.3	260	9	AJ281544	AJ281544	4A3A-P6C9
c 429	19	2.4	931	10	BF163443	601771612	c 502	18	2.3	260	9	BE059056	BE059056	4A3A-P6C9
c 430	19	2.4	956	12	CNS0272U	AL185331	c 503	18	2.3	265	9	AW529484	AW529484	sn24f08.y
c 431	19	2.4	958	12	CNS06PBI	AL409139	c 504	18	2.3	265	12	BH192911	BH192911	UI-R-BT1-
c 432	19	2.4	976	12	CNS035YU	AL223359	c 505	18	2.3	266	10	BE953648	BE953648	TC3-70G7-
c 433	19	2.4	985	12	CNS037SC	AL231717	c 506	18	2.3	273	9	AA819089	AA819089	UI-M-CC1-
c 434	19	2.4	988	10	BE907598	BE907598	c 507	18	2.3	273	9	AV417272	AV417272	UI-R-A0-a
c 435	19	2.4	989	9	A1964363	EST269477	c 508	18	2.3	274	10	BF371887	BF371887	AV417272
c 436	19	2.4	1010	10	BF203342	601865946	c 509	18	2.3	278	12	AQ102939	AQ102939	QV4-F000
c 437	19	2.4	1035	12	AG127413	Pan trogl	c 510	18	2.3	278	12	AQ102939	AQ102939	BS524171
c 438	19	2.4	1094	10	BF306609	601888859	c 511	18	2.3	282	9	AW493262	AW493262	BS524171
c 439	19	2.4	1146	10	EG113345	602284950	c 512	18	2.3	282	10	BF407424	BF407424	UI-M-BH3-
c 440	19	2.4	1164	10	BE618333	601462726	c 513	18	2.3	284	9	BB079171	BB079171	UI-R-BJ2-
c 441	19	2.4	1292	10	BM415039	6020095.M	c 514	18	2.3	288	12	AZ459363	AZ459363	1M0264F12
c 442	19	2.4	1353	10	BE903463	601677729	c 515	18	2.3	288	9	AV555681	AV555681	AV555681
c 443	19	2.4	1403	12	AG060395	AG060395	c 516	18	2.3	290	9	BB337259	BB337259	UI-R-DK0-
c 444	19	2.4	1685	10	BE733622	601565994	c 517	18	2.3	290	9	BB337259	BB337259	BB337259
c 445	19	2.4	1763	10	BF165204	60178071	c 518	18	2.3	290	9	BB337259	BB337259	BB337259
c 446	19	2.4	1827	10	BI489151	603021259	c 519	18	2.3	291	9	AV160063	AV160063	AV160063
c 447	19	2.4	1953	10	BF026022	601670339	c 520	18	2.3	291	9	AV427352	AV427352	AV427352
c 448	19	2.4	2160	10	EG024074	602303119	c 521	18	2.3	291	9	BB485672	BB485672	BB485672
c 449	18	2.3	118	9	AW491438	AV415847	c 522	18	2.3	291	10	BE476222	BE476222	158852.BA
c 450	18	2.3	122	9	AV415847	AV415847	c 523	18	2.3	293	9	AI837074	AI837074	UI-M-AK0-
c 451	18	2.3	123	9	AV427993	AV427993	c 524	18	2.3	293	9	AV128333	AV128333	AV128333
c 452	18	2.3	125	10	BI671551	fs49g05.y	c 525	18	2.3	293	9	BB555850	BB555850	BB555850
c 453	18	2.3	132	10	BF469705	UI-M-BH3-	c 526	18	2.3	296	9	AV118678	AV118678	AV118678
c 454	18	2.3	140	10	BI714151	1e33e12.x	c 527	18	2.3	300	12	BH618245	BH618245	SALR_0387
c 455	18	2.3	144	9	AW159612	z604g05.x	c 528	18	2.3	301	12	AQ095016	AQ095016	HS_3028_A

675	18	2.3	433	9	BE172782	BE172782	MRO-HT055	748	18	2.3	495	9	AW500337	AW500337	UI-HF-BNO
c 676	18	2.3	435	9	AW523833	AW523833	UI-R-BJOP	c 749	18	2.3	496	10	BG632704	BG632704	GHI2617.3
c 677	18	2.3	435	9	BE061545	BE061545	MRO-BT024	c 750	18	2.3	496	12	AZ438612	AZ438612	1M0228J14
678	18	2.3	437	9	AW456686	AW456686	UI-M-BH3-	c 751	18	2.3	497	9	AL119550	AL119550	DKEZP761B
679	18	2.3	440	9	AV406890	AV406890	AV406890	c 752	18	2.3	497	12	AZ719287	AZ719287	RPCI-24-1
680	18	2.3	441	9	AV739205	AV739205	AV739205	c 753	18	2.3	502	9	AI483446	AI483446	EST249267
c 681	18	2.3	441	10	BG942075	BG942075	ax20911.x	c 754	18	2.3	502	10	BM383708	BM383708	UI-R-DM1-
682	18	2.3	442	9	AI182988	AI182988	AUI82988	c 755	18	2.3	504	9	AI485030	AI485030	EST243310
683	18	2.3	444	9	AV429135	AV429135	AV429135	c 756	18	2.3	504	10	BG514253	BG514253	G94904.x
c 684	18	2.3	447	9	AI072445	AI072445	UI-R-C2-n	c 757	18	2.3	505	10	BI315894	BI315894	SAF64902.
c 685	18	2.3	447	9	BE061565	BE061565	MRO-BT024	c 758	18	2.3	506	9	AI138041	AI138041	UI-R-C2p-
c 686	18	2.3	448	9	AW938394	AW938394	PM4-DT005	c 759	18	2.3	508	10	BE646204	BE646204	7683a06.x
c 687	18	2.3	448	9	BE061570	BE061570	MRO-BT024	c 760	18	2.3	508	12	AI016782	AI016782	HS.2224.B
c 688	18	2.3	448	9	BE061599	BE061599	MRO-BT024	c 761	18	2.3	510	10	BI298738	BI298738	UI-R-CV2-
c 689	18	2.3	451	9	AI043907	AI043907	UI-R-C0-j	c 762	18	2.3	511	9	AA437284	AA437284	zv62b11.s
c 690	18	2.3	451	9	AW045648	AW045648	UI-M-BH1-	c 763	18	2.3	511	10	H23095	H23095	ym51d10.r1
c 691	18	2.3	452	9	BE061594	BE061594	MRO-BT024	c 764	18	2.3	511	12	AI0183788	AI0183788	HS.3199.B
c 692	18	2.3	452	9	BE099693	BE099693	UI-R-BJ1-	c 765	18	2.3	512	10	BG685618	BG685618	602637596
693	18	2.3	452	10	BE448487	BE448487	ut-90e05.y	c 766	18	2.3	513	10	BE464656	BE464656	hs86b02.x
694	18	2.3	454	9	AV423526	AV423526	AV423526	c 767	18	2.3	514	12	AZ223556	AZ223556	RPCI-23-7
c 695	18	2.3	454	9	AV763938	AV763938	AV763938	c 768	18	2.3	515	10	BE408313	BE408313	601302313
c 696	18	2.3	454	9	BE061496	BE061496	MRO-BT024	c 769	18	2.3	515	12	AZ366375	AZ366375	1M0115005
697	18	2.3	454	10	BI809999	BI809999	1001A11.O	c 770	18	2.3	516	12	AQ392326	AQ392326	CITBI-E1-
698	18	2.3	454	10	T47182	T47182	y653d10.r1	c 771	18	2.3	517	10	C96939	C96939	C96939 Rice
c 699	18	2.3	455	9	AI622350	AI622350	486040E05	c 772	18	2.3	518	12	AQ731916	AQ731916	HS.5548.A
c 700	18	2.3	455	9	AV423492	AV423492	AV423492	c 773	18	2.3	519	10	BF410145	BF410145	UI-R-CAL-
c 701	18	2.3	455	9	AW323244	AW323244	uo57h06.y	c 774	18	2.3	521	9	BE116156	BE116156	UI-R-BS1-
c 702	18	2.3	456	9	AI314818	AI314818	u31903.x	c 775	18	2.3	521	10	H08295	H08295	y192b02.r1
c 703	18	2.3	456	9	AI0181310	AI0181310	AI0181310	c 776	18	2.3	522	9	AL598904	AL598904	DKRZP313C
c 704	18	2.3	456	9	BE146010	BE146010	MRO-HT020	c 777	18	2.3	525	9	AI733033	AI733033	oj28d01.x
c 705	18	2.3	456	10	BF405710	BF405710	UI-R-CAL-	c 778	18	2.3	525	10	BM080277	BM080277	MEST106-D
c 706	18	2.3	457	10	BF419597	BF419597	UI-R-CAO-	c 779	18	2.3	525	12	AZ063489	AZ063489	RPCI-23-4
c 707	18	2.3	457	10	BF510908	BF510908	UI-H-B14-	c 780	18	2.3	525	12	AZ261475	AZ261475	RPCI-23-1
c 708	18	2.3	458	9	AW036862	AW036862	614019G07	c 781	18	2.3	527	10	R60415	R60415	yh04h05.r1
c 709	18	2.3	459	9	AI397761	AI397761	NCC5A477	c 782	18	2.3	528	9	AL380082	AL380082	MtBB50C09
c 710	18	2.3	459	9	BE146194	BE146194	MRO-HT020	c 783	18	2.3	530	10	BE628786	BE628786	uo08a06.x
c 711	18	2.3	461	10	BI300463	BI300463	UI-R-CV2-	c 784	18	2.3	531	10	H15326	H15326	ym28d07.r1
712	18	2.3	462	9	AI089922	AI089922	qai6c08.x	c 785	18	2.3	531	12	AZ504695	AZ504695	1M0345D02
713	18	2.3	462	9	AV422721	AV422721	AV422721	c 786	18	2.3	533	10	BM127376	BM127376	1698a08.x
714	18	2.3	462	9	AV423381	AV423381	AV423381	c 787	18	2.3	533	10	H24417	H24417	ym53f12.r1
715	18	2.3	463	10	BI810919	BI810919	K011C02.O	c 788	18	2.3	533	12	B07921	B07921	pbAC.3.5.re
716	18	2.3	463	12	AO083076	AO083076	RPCI11-56	c 789	18	2.3	533	12	AO458440	AO458440	HS.5207.A
c 717	18	2.3	464	10	BF461828	BF461828	UI-M-CG0P	c 790	18	2.3	534	10	EG181416	EG181416	RST260.A
c 718	18	2.3	465	10	EG399981	EG399981	602442035	c 791	18	2.3	534	12	CNS00NRV	AL082297	Arabi0ops
c 719	18	2.3	466	9	AI721737	AI721737	fc31910.x	c 792	18	2.3	536	10	BM420236	BM420236	U004G05.O
720	18	2.3	467	9	AW500274	AW500274	UI-HF-BNO	c 793	18	2.3	539	12	AQ784867	AQ784867	HS.3180.A
c 721	18	2.3	467	10	BI809789	BI809789	G002G03.O	c 794	18	2.3	539	12	AZ271211	AZ271211	RPCI-23-1
c 722	18	2.3	468	10	R17192	R17192	yq11d05.r1	c 795	18	2.3	540	10	BJ176566	BJ176566	BJ176566
c 723	18	2.3	470	10	BM419464	BM419464	R014B04.O	c 796	18	2.3	540	10	BM379543	BM379543	MEST507-A
c 724	18	2.3	471	9	BE146012	BE146012	MRO-HT020	c 797	18	2.3	543	9	AI398117	AI398117	NCSM2F11T
c 725	18	2.3	472	9	AV422843	AV422843	AV422843	c 798	18	2.3	543	9	AW128371	AW128371	fc38f07.x
727	18	2.3	474	9	BE146072	BE146072	MRO-HT020	c 799	18	2.3	544	9	AI103454	AI103454	EST212743
727	18	2.3	475	12	AZ429457	AZ429457	1M0213J21	c 800	18	2.3	544	9	AI485939	AI485939	EST244260
728	18	2.3	475	12	AZ657376	AZ657376	1M0533G04	c 801	18	2.3	548	9	AW438183	AW438183	707066E03
c 729	18	2.3	478	9	AO095018	AO095018	AO095018	c 802	18	2.3	548	12	AO519123	AO519123	HS.5150.B
c 730	18	2.3	478	10	BI118684	BI118684	EST070.D1	c 803	18	2.3	550	12	AZ282429	AZ282429	RPCI-23-1
c 731	18	2.3	478	12	AQ334072	AQ334072	HS.5010.A	c 804	18	2.3	552	9	BE100176	BE100176	UI-R-BJ1-
c 732	18	2.3	479	10	H27819	H27819	y162c04.r1	c 805	18	2.3	553	10	BI887123	BI887123	z16337-1-0
c 733	18	2.3	480	12	AQ634317	AQ634317	RPCI-11-4	c 806	18	2.3	553	12	AO965179	AO965179	LERIA79TR
734	18	2.3	481	12	AQ280653	AQ280653	CITBI-E1-	c 807	18	2.3	553	12	BH315597	BH315597	CH230-196
735	18	2.3	482	9	BB760911	BB760911	BB760911	c 808	18	2.3	555	9	AW145607	AW145607	AU145607
c 736	18	2.3	482	10	BF393956	BF393956	UI-R-CAO-	c 809	18	2.3	555	12	AO342749	AO342749	RPCI11-11
c 737	18	2.3	483	10	BF386286	BF386286	UI-R-CAL-	c 810	18	2.3	557	10	BE810064	BE810064	218865.WA
c 738	18	2.3	484	10	BG893169	BG893169	daa89C04.	c 811	18	2.3	558	10	BJ174299	BJ174299	BU174299
c 739	18	2.3	484	10	BI841661	BI841661	ft03c08.x	c 812	18	2.3	559	12	BI197407	BI197407	TC3-70D18
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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VERSION     BE881023.1 GI:10329799
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SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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http://image.llnl.gov
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Location/Qualifiers

FEATURES

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Technologies."
Location/Qualifiers

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Qy 576 AACACCGGGGATAAATCTGGATTTGGGTTCGGGGTCAAGGTGAAGATAATACCTAAAGA 635
Db 301 AACACCGGGGATAAATCTGGATTTGGGTTCGGGGTCAAGGTGAAGATAATACCTAAAGA 360
Qy 636 GGAACACTGTAATGCCAGAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGACAAG 695
Db 361 GGAACACTGTAATGCCAGAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGACAAG 420
Qy 696 CTGAACAACCAAGCTGTTTATATTAGATATTGACTTAAACTATCTCAATAAAGTT 755
Db 421 CTGAACAACCAAGCTGTTTATATTAGATATTGACTTAAACTATCTCAATAAAGTT 480
Qy 756 TTGCAGCTT 764
Db 481 TTGCAGCTT 489

RESULT 3
BI460303
LOCUS 603201939f1 NIH_MGC_97 Homo sapiens cdna linear ESR 21-AUG-2001
DEFINITION mRNA sequence.
BI460303
ACCESSION BI460303.1 GI:15250959
VERSION EST
KEYWORDS human.
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 486)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11675 row: n column: 10
High quality sequence stop: 486.
Location/Qualifiers

FEATURES

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1. .486
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/db_xref="taxon:9606"
/clone="IMAGE:5267913"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTN-3',
size-selected for average insert size 2.2 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
Location/Qualifiers

BASE COUNT 166 a 111 c 123 g 86 t

Query Match 49.9%; Score 390; DB 10; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.1e-130;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 392 GACACACAAACACAGACACAGCCAGTCCAGGAGCCAGTAATGGAGAGCCCCA 451
Db 81 GACACACAAACACAGACACAGCCAGTCCAGGAGCCAGTAATGGAGAGCCCCA 140
Qy 452 AAAAGAAGAACACAG..TGAAAGTCGGGATCCTACACCTGGGCGAGCAGACAGAGAAGA 511
Db 141 AAAAGAAGAACACAGCTGAAAGTCGGGATCCTACACCTGGGCGAGCAGACAGAGAAGA 200
Qy 512 TCAGGATACAGCTCAGATCCAGTCCGGGACATGGAAGGTGATCTGCAAGAGCTGCATCA 571
Db 201 TCAGGATACAGCTCAGATCCAGTCCGGGACATGGAAGGTGATCTGCAAGAGCTGCATCA 260
Qy 572 GTCAAAACACCGGGGATAAATCTGGATTTGGGTTCGGGGTCAAGGTGAAGATAATACCTA 631
Db 261 GTCAAAACACCGGGGATAAATCTGGATTTGGGTTCGGGGTCAAGGTGAAGATAATACCTA 320
Qy 632 AAGAGAACACTGTAAATGCCAGAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGA 691
Db 321 AAGAGAACACTGTAAATGCCAGAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGA 380
Qy 692 CAAGCTGAACACGCGAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATAA 751
Db 381 CAAGCTGAACACGCGAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATAA 440
Qy 752 AGTTTTCAGCTTTTCACCAAAAAA 781
Db 441 AGTTTTCAGCTTTTCACCAAAAAA 470

RESULT 4
BG772292
LOCUS BG772292 487 bp mRNA linear EST 15-MAY-2001
DEFINITION 602722580f1 NIH_MGC_97 Homo sapiens cdna clone IMAGE:4839426 5',
mRNA sequence.
ACCESSION BG772292
VERSION BG772292.1 GI:14082945

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS 1 (bases 1 to 487)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: Miklos Paikovitcs, M.D., Ph.D.
CDNA Library preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10774 row: p column: 19
High quality sequence stop: 483.
Location/Qualifiers
1. .487
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4839426"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcagag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 166 a 113 c 123 g 85 t
ORIGIN
Query Match 49.9%; Score 390; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.1e-130;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 392 GACACACAAACACAGAGCCAGTCCAGGAGCCAGTAAATGGAGAGCCCA 451
Db 81 GACACACAAACACAGAGCCAGTCCAGGAGCCAGTAAATGGAGAGCCCA 140
QY 452 AAAAGAAGAACACAGAGTGAAGTCCGGATCCTACACCTGGCGAGCAGACAGCAAGA 511
Db 141 AAAAGAAGAACACAGAGTGAAGTCCGGATCCTACACCTGGCGAGCAGACAGCAAGA 200
QY 512 TCAGGATACAGCTGAGATCCAGTCCGCGACATGGAAGTGTATCTGCAAGAGCTGCATCA 571
Db 201 TCAGGATACAGCTGAGATCCAGTCCGCGACATGGAAGTGTATCTGCAAGAGCTGCATCA 260
QY 572 GTCAACACCCGGGATAATCTGGATTGGTTCCGGCGTCAAGTGAAGATAATACCTA 631
Db 261 GTCAACACCCGGGATAATCTGGATTGGTTCCGGCGTCAAGTGAAGATAATACCTA 320
QY 632 AAGAGGAACACTGTAATAATGCCAGAGCAGGTGAAGAGCAACACACAAAGTTTAAATGAAGA 691
Db 321 AAGAGGAACACTGTAATAATGCCAGAGCAGGTGAAGAGCAACACACAAAGTTTAAATGAAGA 380
QY 692 CAAGCTGAACACGCAAGCTGTTTTATATTAGATATTGTGACTTAAACTATCTCAATAA 751
Db 381 CAAGCTGAACACGCAAGCTGTTTTATATTAGATATTGTGACTTAAACTATCTCAATAA 440
QY 752 AGTTTTGCAGCTTTCACCAAAAAA 781
Db 441 AGTTTTGCAGCTTTCACCAAAAAA 470

RESULT 5
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LOCUS
DEFINITION BE876234 880 bp mRNA linear EST 20-OCT-2000
601486758F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889095 5',
mRNA sequence.
ACCESSION BE876234
VERSION BE876234.1 GI:10325114
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 880)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: DCTD/BTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9670 row: c column: 16
High quality sequence stop: 493.
Location/Qualifiers
1. .880
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/db_xref="taxon:9606"
/clone="IMAGE:3889095"
/clone_lib="NIH_MGC_69"
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT 382 a 192 c 209 g 97 t
ORIGIN
Query Match 49.9%; Score 390; DB 10; Length 880;
Best Local Similarity 100.0%; Pred. No. 8.1e-131;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 392 GACACACAAACACAGAACACACAGCCAGTCCAGGAGCCAGTAAATGGAGAGCCCA 451
Db 64 GACACACAAACACAGAACACACAGCCAGTCCAGGAGCCAGTAAATGGAGAGCCCA 123
QY 452 AAAAGAAGAACACAGAGTGAAGTCCGGATCCTACACCTGGCGAGCAGACAGCAAGAAGA 511
Db 124 AAAAGAAGAACACAGAGTGAAGTCCGGATCCTACACCTGGCGAGCAGACAGCAAGAAGA 183
QY 512 TCAGGATACAGCTGAGATCCAGTCCGCGACATGGAAGTGTATCTGCAAGAGCTGCATCA 571
Db 184 TCAGGATACAGCTGAGATCCAGTCCGCGACATGGAAGTGTATCTGCAAGAGCTGCATCA 243
QY 572 GTCAACACCCGGGATAATCTGGATTGGTTCCGGCGTCAAGTGAAGATAATACCTA 631
Db 244 GTCAACACCCGGGATAATCTGGATTGGTTCCGGCGTCAAGTGAAGATAATACCTA 303
QY 632 AAGAGGAACACTGTAATAATGCCAGAGCAGGTGAAGAGCAACACACAAAGTTTAAATGAAGA 691
Db 304 AAGAGGAACACTGTAATAATGCCAGAGCAGGTGAAGAGCAACACACAAAGTTTAAATGAAGA 363
QY 692 CAAGCTGAACACGCAAGCTGTTTTATATTAGATATTGTGACTTAAACTATCTCAATAA 751
Db 364 CAAGCTGAACACGCAAGCTGTTTTATATTAGATATTGTGACTTAAACTATCTCAATAA 423
QY 752 AGTTTTGCAGCTTTCACCAAAAAA 781
Db 424 AGTTTTGCAGCTTTCACCAAAAAA 453

RESULT 6
 AA948244/c
 LOCUS
 DEFINITION
 AA948244
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 428)
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40ml3 fwd. ET from Amersham.
 Location/Qualifiers
 1..428
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1588176"
 /clone_lib="NCI-CCAP_GC4"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from 3 pooled
 germ cell tumors, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT7T3
 vector. Library is normalized. Library was constructed by
 Bento Soares and M. Fatima Bonaldo."
 80 a 104 c 99 g 145 t
 BASE COUNT
 ORIGIN
 Query Match 48.5%; Score 379; DB 9; Length 428;
 Best Local Similarity 100.0%; Pred. No. 1.1e-126;
 Mismatches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 392 GACACACAAACACAGAACCCACAGCCAGTCCCAGGAGCCAGTAATGGAGAGCCCCA 451
 Db 379 GACACACAAACACAGAACCCACAGCCAGTCCCAGGAGCCAGTAATGGAGAGCCCCA 320
 QY 452 AAAGAAGAACACAGCAGTGAAGTCGGGATCTTACACCTGGCAGCAGACAGAGA 511
 Db 319 AAAGAAGAACACAGCAGTGAAGTCGGGATCTTACACCTGGCAGCAGACAGAGA 260
 QY 512 TCAGGATACAGCTGAGATCCCAAGTCGCCACATGGAAGTGATCTGCAAGAGCTGCATCA 571
 Db 259 TCAGGATACAGCTGAGATCCCAAGTCGCCACATGGAAGTGATCTGCAAGAGCTGCATCA 200
 QY 572 GTCAACACCGGGGATAAATCTGGATTTTGGGTTCCGGCTCAAGGTGAAGATAAATACCTA 631
 Db 199 GTCAACACCGGGGATAAATCTGGATTTTGGGTTCCGGCTCAAGGTGAAGATAAATACCTA 140
 QY 632 AAGAGAACACTGTAAATGCCAAGAGCAGGTGAAGAGCAACACCAAGTTTAAATGAAGA 691
 Db 139 AAGAGAACACTGTAAATGCCAAGAGCAGGTGAAGAGCAACACCAAGTTTAAATGAAGA 80

QY 692 CAAGCTGAACCAACGCAAGCTGGTTTATATTAGATATTTGACTTAACTATCTCAATAA 751
 Db 79 CAAGCTGAACCAACGCAAGCTGGTTTATATTAGATATTTGACTTAACTATCTCAATAA 20
 QY 752 AGTTTTCAGCTTTTCACCA 770
 Db 19 AGTTTTCAGCTTTTCACCA 1
 RESULT 7
 AA620697/c
 LOCUS
 DEFINITION
 af89401.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1049185
 3', mRNA sequence.
 AA620697
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 414)
 Hillier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
 Krizman D., Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin
 J., Moore B., Schellenberg K., Steptoe M., Tan F., Theising B.,
 White Y., Wyllie T., Waterston R. and Wilson R.
 WashU-NCI human EST Project
 Unpublished (1997)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 375.
 Location/Qualifiers
 1..414
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 /db_xref="taxon:9606"
 /clone="IMAGE:1049185"
 /clone_lib="Soares_testis_NHT"
 /sex="male"
 /lab_host="DH10B"
 /note="vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech Laboratories
 Inc., and primed with a Not I - oligo(dT) primer [5',
 TGTACCAATCTGAAGTGGCAGCGCGCCCAATTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7T3 vector. Library
 went through one round of normalization to Col5, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 77 a 100 c 94 g 143 t
 BASE COUNT
 ORIGIN
 Query Match 48.4%; Score 378; DB 9; Length 414;
 Best Local Similarity 100.0%; Pred. No. 2.5e-126;
 Mismatches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 392 GACACACAAACACAGAACCCACAGCCAGTCCCAGGAGCCAGTAATGGAGAGCCCCA 451
 Db 378 GACACACAAACACAGAACCCACAGCCAGTCCCAGGAGCCAGTAATGGAGAGCCCCA 319
 QY 452 AAAGAAGAACACAGCAGCTGAAGTCGGGATCTTACACCTGGCAGCAGACAGAGAAGA 511
 Db 318 AAAGAAGAACACAGCAGCTGAAGTCGGGATCTTACACCTGGCAGCAGACAGAGAAGA 259
 QY 512 TCAGATACAGCTGAGATCCCAAGTCGCCAGATGGAAGGTGATCTGCAAGAGCTGCATCA 571
 Db 139 TCAGATACAGCTGAGATCCCAAGTCGCCAGATGGAAGGTGATCTGCAAGAGCTGCATCA 571

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Db 258 TCAGGATACAGCTGAGATCCCACTGCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCA 199
QY 572 GTCAACACCGGGGATAAATCTCGATTGGTTCCGGCGTCAAGGTGAAGATAATACCTA 631
Db 198 GTCAACAACGCGGGATAAATCTCGATTGGTTCCGGCGTCAAGGTGAAGATAATACCTA 139
QY 632 AAGAGGAACACTGTAAATGCCAGAGCAGGTGAAGAGCAACACAAAGTTTAAATGAAGA 691
Db 138 AAGAGGAACACTGTAAATGCCAGAGCAGGTGAAGAGCAACACAAAGTTTAAATGAAGA 79
QY 692 CAAGCTGAACACGCAAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATA 751
Db 78 CAAGCTGAACACGCAAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATA 19
QY 752 AGTTTTCAGCTTTCACC 769
Db 18 AGTTTTCAGCTTTCACC 1

RESULT 8
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LOCUS wq32c10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2472978 3',
DEFINITION mRNA sequence.
ACCESSION AI954712
VERSION AI954712.1 GI:5747022
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 438)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbbrp/image/image.html
Insert length: 536 Std Error: 0.00
Seq primer: -40UP from Gibco.
FEATURES
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1..438
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2472978"
/tissue_type="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker. Site1: Not I; Site2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP_GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clones
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 79 a 104 c 97 g 158 t
ORIGIN
Query Match 47.0%; Score 367; DB 9; Length 438;
Best Local Similarity 100.0%; Pred. No. 2.3e-122;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 392 GACACACAAAAACACAGAACCCACACAGCCAGTCCCAAGAGCCAGTAATGGAGAGCCCCA 451
Db 391 GACACACAAAAACACAGAACCCACACAGCCAGTCCCAAGAGCCAGTAATGGAGAGCCCCA 332
QY 452 AAAAGAAGAACCCACAGCAGCTGAAAGTCGGATCCTACACCTGGGCAGCAGACAGAAGA 511
Db 331 AAAAGAAGAACCCACAGCAGCTGAAAGTCGGATCCTACACCTGGGCAGCAGACAGAAGA 272
QY 512 TCAGGATACAGCTGAGATCCCACTGCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCA 571
Db 271 TCAGGATACAGCTGAGATCCCACTGCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCA 212
QY 572 GTCAACACCGGGGATAAATCTGGATTTCGGCTCCCGCTCAAGGTGAAGATAATACCTA 631
Db 211 GTCAACACCGGGGATAAATCTGGATTTCGGCTCCCGCTCAAGGTGAAGATAATACCTA 152
QY 632 AAGAGGAACACTGTAAATGCCAGAGCAGGTGAAGAGCAACACAAAGTTTAAATGAAGA 691
Db 151 AAGAGGAACACTGTAAATGCCAGAGCAGGTGAAGAGCAACACAAAGTTTAAATGAAGA 92
QY 692 CAAGCTGAACACGCAAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATA 751
Db 91 CAAGCTGAACACGCAAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATA 32
QY 752 AGTTTTCAGCTTTCACC 758
Db 31 AGTTTTCAGCTTTCACC 25

RESULT 9
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LOCUS 601483262F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:388585 5',
DEFINITION mRNA sequence.
ACCESSION BE620196
VERSION BE620196.1 GI:9891134
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1140)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9661 row: 1 column: 16
High quality sequence stop: 440.
FEATURES
Location/Qualifiers
1..1140
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:388585"
/tissue_type="NIH_MGC_69"
/lab_host="NIH_MGC_69"
/notes="Organ: lung; Vector: PCWV-SPORT6; Site1: NotI;
Site2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT 540 a 242 c 266 g 90 t 2 others
ORIGIN
Query Match 46.1%; Score 360; DB 10; Length 1140;
Best Local Similarity 100.0%; Pred. No. 4.6e-120;

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QY 408 GAACACACAGCCAGTCCAGGAGCCAGTAATGGAGAGCCCAAAAGAAAGAACAGCA 467
Db 1 GAACACACAGCCAGTCCAGGAGCCAGTAATGGAGAGCCCAAAAGAAAGAACAGCA 60
QY 468 GCTGAAAGTCGGGATCTACACCTGGGCGAGCAGACAGAAAGATCAGGATACAGCTGAG 527
Db 61 GCTGAAAGTCGGGATCTACACCTGGGCGAGCAGACAGAAAGATCAGGATACAGCTGAG 120
QY 528 ATCCAGTCGCGGACATGGAAGTGATCTGCAAGAGCTGCATCAGTCAAAACCCGGGGAT 587
Db 121 ATCCAGTCGCGGACATGGAAGTGATCTGCAAGAGCTGCATCAGTCAAAACCCGGGGAT 180
QY 588 AAATCTGGATTTGGGTTTCGGCGCTCAAGGTGAAGTAATAACCTAAAGAGAAACACTGTAA 647
Db 181 AAATCTGGATTTGGGTTTCGGCGCTCAAGGTGAAGTAATAACCTAAAGAGAAACACTGTAA 240
QY 648 AATGCCAGACAGCTCAAGCAACACACAAAGTTTAAATCAAGCAAGCTGAAACAGGC 707
Db 241 AATGCCAGACAGCTCAAGCAACACACAAAGTTTAAATCAAGCAAGCTGAAACAGGC 300
QY 708 AAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATAAAGTTTTCAGCTTTTCA 767
Db 301 AAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATAAAGTTTTCAGCTTTTCA 360

RESULT 10
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LOCUS wb08d02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2305059 3',
DEFINITION mRNA sequence.
ACCESSION AT631681
VERSION AT631681.1 GI:4683011
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 421)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: rcapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/hrbp/image/image.html
Insert Length: 515 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .421
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2305059"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="vector: pT7D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
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BASE COUNT 75 a 96 c 95 g 155 t
ORIGIN
Query Match 46.0%; Score 359; DB 9; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.8e-119;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 392 GACACACAAACACAGAACCCACAGCCAGTCCAGGAGCCCAATATGGAGAGCCCCA 451
Db 393 GACACACAAACACAGAACCCACAGCCAGTCCAGGAGCCCAATATGGAGAGCCCCA 334
QY 452 AAAAGAAGAACACAGCAGCTGAAAGTCGGGATCTTACCTGGGCGAGCAGACAGAAAGA 511
Db 333 AAAAGAAGAACACAGCAGCTGAAAGTCGGGATCTTACCTGGGCGAGCAGACAGAAAGA 274
QY 512 TCAGGATACAGCTGAGATCCCGAGTCGGGACATGGAAGTGATCTGCAAGAGCTGCATCA 571
Db 273 TCAGGATACAGCTGAGATCCCGAGTCGGGACATGGAAGTGATCTGCAAGAGCTGCATCA 214
QY 572 GTCAACACCCGGGATAAATCTGGATTTGGGTTCCGGGCTCAAGGTGAAGATAATACCTA 631
Db 213 GTCAACACCCGGGATAAATCTGGATTTGGGTTCCGGGCTCAAGGTGAAGATAATACCTA 154
QY 632 AAGAGGAACACTGTAAATGCCAGAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGA 691
Db 153 AAGAGGAACACTGTAAATGCCAGAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGA 94
QY 692 CAAGCTGAAACACGCAAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATA 750
Db 93 CAAGCTGAAACACGCAAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATA 35

RESULT 11
AW975988
LOCUS EST38097 MAGE resequences, MAGN Homo sapiens cDNA, mRNA sequence.
DEFINITION AW975988
VERSION AW975988.1 GI:8167210
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 556)
Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 355
Seq primer: Forward.
Location/Qualifiers
1. .556
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGN"
/note="Vector: pBluescriptSKM"
BASE COUNT 168 a 125 c 145 g 118 t
ORIGIN
Query Match 43.3%; Score 338; DB 9; Length 556;
Best Local Similarity 100.0%; Pred. No. 5.6e-112;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 433 CCAGTAATGGAGAGCCCCCAAAAGAAAGAACACAGCAGCTGAAAGTCGGGATCTTACACCTG 492
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Db 94  CCAGTAATGAGAGCCCAAAAAAGAAAGAACACGACGCTGAAAGTCGGGATCCTTACACCTG 153
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Qy 493  GGCAGCAGACAGAAAGATGACGATACAGCTGAGATCCAGTGCCGCGACATGGAAGGTG 552
      |||
Db 154  GGCAGCAGACAGAAAGATGACGATACAGCTGAGATCCAGTGCCGCGACATGGAAGGTG 213
      |||
Qy 553  ATCTGCAAGAGCTGCATCAGTCAAAACACCGGGGATAAATCTGATTTGGGTTCCGGCGTC 612
      |||
Db 214  ATCTGCAAGAGCTGCATCAGTCAAAACACCGGGGATAAATCTGATTTGGGTTCCGGCGTC 273
      |||
Qy 613  AAGGTGAAGATAATACCTAAAGAGGACACTGTAATGTCACAGCAAGCGTGAAGACAA 672
      |||
Db 274  AAGGTGAAGATAATACCTAAAGAGGACACTGTAATGTCACAGCAAGCGTGAAGACAA 333
      |||
Qy 673  CCACAAGTTTAAATGAAGACAAAGCTGAAACACGCAAGCTGGTTTATATTAGATATTG 732
      |||
Db 334  CCACAAGTTTAAATGAAGACAAAGCTGAAACACGCAAGCTGGTTTATATTAGATATTG 393
      |||
Qy 733  ACTTAAACTATCAATAAAGTTTTCGAGCTTTCACCA 770
      |||
Db 394  ACTTAAACTATCAATAAAGTTTTCGAGCTTTCACCA 431
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RESULT 12
AA648117/c
LOCUS      AA648117      423 bp      mRNA      linear      EST 13-NOV-1997
DEFINITION ns06407.r1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182829, mRNA
sequence.
ACCESSION  AA648117
VERSION     AA648117.1  GI:2574546
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 423)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
             Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html
             Insert Length: 599 Std Error: 0.00
             Seq primer: -28m13 rev1 Et from Amersham
             High quality sequence stop: 408.
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             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="IMAGE:1182829"
             /clone_lib="NCI_CGAP_Ew1"
             /tissue_type="Ewing's sarcoma"
             /lab_host="DH10B"
             /note="Vector: pAMP10; mRNA made from Ewing's sarcoma,
             cDNA made by oligo-dT priming. Non-directionally cloned.
             Size-selected on agarose gel, average insert size 600 bp.
             Reference: Krizman et al. (1996) Cancer Research
             56:5380-5383."
BASE COUNT  77 a 101 c 90 g 155 t
ORIGIN
Query Match 42.9%; Score 335; DB 9; Length 423;
Best Local Similarity 99.7%; Pred. No. 7.8e-111;
Matches 385; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 392  GACACACAAACACAGAACCCACACAGCCAGTCCCGAGGAGCCAGTAATGGAGAGCCCCA 451
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Db 415  GACACACAAACACAGAACCCACACAGCCAGTCCCGAGGAGCCAGTAATGGAGAGCCCCA 356
      |||
Qy 452  AAAGAAGAANCACAGCAGCTGAAAGTCGGATCCTACACCTGGCGACGACACAGAAGA 511
      |||
Db 355  AACAGAAGAANCACAGCAGCTGAAAGTCGGATCCTACACCTGGCGACGACACAGAAGA 245
      |||
Qy 512  TCAGGATACAGCTGAGATCCCGAGTCGCGACATGGAAGTGATCTCCAAGAGCTGCATCA 571
      |||
Db 295  TCAGGATACAGCTGAGATCCCGAGTCGCGACATGGAAGTGATCTCCAAGAGCTGCATCA 236
      |||
Qy 572  GTCAAACACCGGGGATAAATCTGGATTTGGGTTCCGGCGTCAAGGTGAAGATAATACCTA 631
      |||
Db 235  GTCAAACACCGGGGATAAATCTGGATTTGGGTTCCGGCGTCAAGGTGAAGATAATACCTA 176
      |||
Qy 632  AGAGGAACACACTGTTAAATGCCAGAAGCAGGTGAAGCAACACACAAGTTTAAATCAAGA 691
      |||
Db 175  AGAGGAACACACTGTTAAATGCCAGAAGCAGGTGAAGCAACACACAAGTTTAAATCAAGA 116
      |||
Qy 692  CAAGCTGAAACAAACGCAAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATAA 751
      |||
Db 115  CAAGCTGAAACAAACGCAAGCTGGTTTATATTAGATATTGACTTAAACTATCTCAATAA 56
      |||
Qy 752  AGTTTTCGAGCTTTCACCAAAAAAAA 777
      |||
Db 55  AGTTTTCGAGCTTTCACCAAAAAAAA 30
      |||

RESULT 13
AA758618/c
LOCUS      AA758618      407 bp      mRNA      linear      EST 23-JAN-1998
DEFINITION ah58d07.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309837 3',
mRNA sequence.
ACCESSION  AA758618
VERSION     AA758618.1  GI:2806481
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 407)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
             , Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html
             Seq primer: -40m13 fwd. Et from Amersham
             High quality sequence stop: 401.
FEATURES
             Location/Qualifiers
             1..407
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone_lib="Soares_testis_NHT"
             /sex="male"
             /lab_host="DH10B"
             /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
             polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
             was prepared from mRNA obtained from Clontech Laboratories
             , Inc., and primed with a Not I - oligo(dT) primer [5',
             TGTTACCAATCTGAAGTGGAGCGCCGCCCAATTTTTTTTTTTT 3'].
             Double-stranded cDNA was ligated to Eco RI adaptors
             (Pharmacia), digested with Not I and cloned into the Not I
```

and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT	77 a	97 c	91 g	142 t		
ORIGIN						
Query Match	39.7%	Score 310;	DB 9;	Length 407;		
Best Local Similarity	100.0%	Pred. No. 8.1e-102;				
Matches 310;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	392	GACACACAAACACAGAACACACAGCCAGTCCAGGAGGCCAGTAAATGAGAGCCCCA	451			
Db	378	GACACACAAACACAGAACACACAGCCAGTCCAGGAGGCCAGTAAATGAGAGCCCCA	319			
QY	452	AAAGAAAGAACACAGCAGTGAAGTCGGATCTACACCTCGGCAGCAGACAGAGAAGA	511			
Db	318	AAAGAAAGAACACAGCAGTGAAGTCGGATCTACACCTCGGCAGCAGACAGAGAAGA	259			
QY	512	TCAGGATACAGCTGAGATCCAGTCGCGGACATGAAGGTGATCTGCAAGAGTGCATCA	571			
Db	258	TCAGGATACAGCTGAGATCCAGTCGCGGACATGAAGGTGATCTGCAAGAGTGCATCA	199			
QY	572	GTCAACACCGGGGATAATCTGGATTTCGGTTCCGGCGTCAAGGTGAAGATAATACCTA	631			
Db	198	GTCAACACCGGGGATAATCTGGATTTCGGTTCCGGCGTCAAGGTGAAGATAATACCTA	139			
QY	632	AAGAGGAACACTGTAATAATGCCAAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGA	691			
Db	138	AAGAGGAACACTGTAATAATGCCAAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGA	79			
QY	692	CAAGCTGAAA 701				
Db	78	CAAGCTGAAA 69				
RESULT 14						
LOCUS	BG217244	485 bp	mRNA	linear EST 21-APR-2001		
DEFINITION	RST36946 Athersys RAGE Library Homo sapiens cdna, mRNA sequence.					
ACCESSION	BG217244					
VERSION	BG217244.1	GI:13743265				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
AUTHORS	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,K., Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,k., Offenbacher,J., Danzig,J. and Ducar,M.					
TITLE	Creation of genome-wide protein expression libraries using random activation of gene expression					
JOURNAL	Nat. Biotechnol. 19 (5), 440-445 (2001)					
MEDLINE	21227151					
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@atersys.com High quality sequence stop: 481.					
FEATURES	Location/Qualifiers					
source	1. 485 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Athersys RAGE Library" /cell_line="HT1080" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation					

method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

Query Match	36.9%	Score 288;	DB 10;	Length 485;
Best Local Similarity	99.5%	Pred. No. 6.3e-94;		
Matches 388;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	392	GACACACAAACACAGAACACACAGCCAGTCCAGGAGGCCAGTAAATGAGAGCCCCA	451	
Db	95	GACACACAAACACAGAACACACAGCCAGTCCAGGAGGCCAGTAAATGAGAGCCCCA	154	
QY	452	AAAGAAAGAACACAGCAGTGAAGTCGGATCTACACCTCGGCAGCAGACAGAGAAGA	511	
Db	155	AAAGAAAGAACACAGCAGTGAAGTCGGATCTACACCTCGGCAGCAGACAGAGAAGA	214	
QY	512	TCAAGATACAGCTGAGATCCAGTCGCGGACATGAAGGTGATCTGCAAGAGTGCATCA	571	
Db	215	TCAGGATACAGCTGAGATCCAGTCGCGGACATGAAGGTGATCTGCAAGAGTGCATCA	274	
QY	572	GTCAACACCGGGGATAATCTGGATTTCGGTTCCGGCGTCAAGGTGAAGATAATACCTA	631	
Db	275	GTCAACACCGGGGATAATCTGGATTTCGGTTCCGGCGTCAAGGTGAAGATAATACCTA	334	
QY	632	AAGAGGAACACTGTAATAATGCCAAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGA	691	
Db	335	AAGAGGAACACTGTAATAATGCCAAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGA	394	
QY	692	CAAGCTGAAACACGCAAGCTGTTTATATAGATATTTCACCTTAACCTATCTCAATAA	751	
Db	395	CAAGCTGAAACACGCAAGCTGTTTATATAGATATTTCACCTTAACCTATCTCAATAA	454	
QY	752	AGTTTTCAGCTTTTCACCAAAAAA 781		
Db	455	AGTTTTCAGCTTTTCACCAAAAAA 484		
RESULT 15				
LOCUS	AV682444	665 bp	mRNA	linear EST 16-JAN-2002
DEFINITION	AV682444 GKB Homo sapiens cdna clone GKBACC10 5', mRNA sequence.			
ACCESSION	AV682444			
VERSION	AV682444.1 GI:10284307			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,O., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.			
TITLE	Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)			
MEDLINE	21625106			
COMMENT	Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai.			
FEATURES	Location/Qualifiers			
source	1. .665 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="GKBACC10" /clone_lib="GKB"			

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/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI;"
BASE COUNT      212 a 152 c 152 g 149 t
ORIGIN
Query Match      36.0%; Score 281; DB 9; Length 665;
Best Local Similarity 100.0%; Pred. No. 1.8e-91;
Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 487 CACCTGGGCAGACAGAGAAGATCAGGATACAGCTGAGATCCAGCTGCGGCACATGG 546
Db 1 CACCTGGGCAGACAGAGAAGATCAGGATACAGCTGAGATCCAGCTGCGGCACATGG 60

Qy 547 AAGGTGATCTCAAGAGCTGCATCAGTCAAAACACCGGGGATAAATCTCGATTTGGGTTC 606
Db 61 AAGGTGATCTCAAGAGCTGCATCAGTCAAAACACCGGGGATAAATCTCGATTTGGGTTC 120

Qy 607 GCGTCAAGTGAAGTATACCTAAAGAGGAACACTGTAATGCCAGAACGAGGTCAA 666
Db 121 GCGTCAAGTGAAGTATACCTAAAGAGGAACACTGTAATGCCAGAACGAGGTCAA 180

Qy 667 GAGCAACCAAGTTTAAATGAAGCAAGCTGAAACACGCAAGCTGTTTATATTAGA 726
Db 181 GAGCAACCAAGTTTAAATGAAGCAAGCTGAAACACGCAAGCTGTTTATATTAGA 240

Qy 727 TATTGACTTAACATCTCAATAAGCTTTTCACGCTTCA 767
Db 241 TATTGACTTAACATCTCAATAAGCTTTTCACGCTTCA 281

RESULT 16
LOCUS      BG216048      394 bp mRNA linear EST 21-APR-2001
DEFINITION RST35862 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG216048
VERSION     BG216048.1 GI:13742197
KEYWORDS    human.
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE   1 (bases 1 to 394)
AUTHORS     Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
            Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
            Creation of genome-wide protein expression libraries using random
            activation of gene expression
            Nat. Biotechnol. 19 (5), 440-445 (2001)
            21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 394.
            Location/Qualifiers
            1..394
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="Athersys RAGE Library"
            /cell_line="HT1080"
            /note="See 'Creation of Genome-wide Protein Expression
            Libraries using Random Activation of Gene Expression',
            Nature Biotechnology, in press. Note that even though the
            cell type indicated is HT1080, since a random activation
            method was used, these sequence tags are not necessarily
            expressed in HT1080 under normal circumstances."

FEATURES
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1..394
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BASE COUNT      149 a      85 c      92 g      68 t
ORIGIN
Query Match      35.1%; Score 274; DB 10; Length 394;
Best Local Similarity 100.0%; Pred. No. 7.7e-89;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 440 TGGAGAGCCCCAAAAGAAAGAACAGCAGCTGAAAGTCGGATCCTACACCTGGGCAGCA 499
Db 52 TGGAGAGCCCCAAAAGAAAGAACAGCAGCTGAAAGTCGGATCCTACACCTGGGCAGCA 111

Qy 500 GACAGAAGAAGATCAGGATCAGATCCAGTCCAGTGGCCGACATGGAAGTGATCTGCA 559
Db 112 GACAGAAGAAGATCAGGATCAGATCCAGTCCAGTGGCCGACATGGAAGTGATCTGCA 171

Qy 560 AGAGCTGCATCAGTCAACACCGGGGATAAATCTGGATTTGGGTTCGGCGTCAAGGTGA 619
Db 172 AGAGCTGCATCAGTCAACACCGGGGATAAATCTGGATTTGGGTTCGGCGTCAAGGTGA 231

Qy 620 AGATAATACCTAAAGAGGAACACTGTAATGCCAGAACGAGGTGAAGACCAACCAAG 679
Db 232 AGATAATACCTAAAGAGGAACACTGTAATGCCAGAACGAGGTGAAGACCAACCAAG 291

Qy 680 TTTAAATGAAGACAAGCTGAAACACGCAAGCTG 713
Db 292 TTTAAATGAAGACAAGCTGAAACACGCAAGCTG 325

RESULT 17
LOCUS      BG206865      388 bp mRNA linear EST 21-APR-2001
DEFINITION RST26327 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG206865
VERSION     BG206865.1 GI:13728552
KEYWORDS    human.
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE   1 (bases 1 to 388)
AUTHORS     Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
            Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
            Creation of genome-wide protein expression libraries using random
            activation of gene expression
            Nat. Biotechnol. 19 (5), 440-445 (2001)
            21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 228.
            Location/Qualifiers
            1..388
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="Athersys RAGE Library"
            /cell_line="HT1080"
            /note="See 'Creation of Genome-wide Protein Expression
            Libraries using Random Activation of Gene Expression',
            Nature Biotechnology, in press. Note that even though the
            cell type indicated is HT1080, since a random activation
            method was used, these sequence tags are not necessarily
            expressed in HT1080 under normal circumstances."

BASE COUNT      143 a      83 c      87 g      71 t
ORIGIN
Query Match      33.2%; Score 259; DB 10; Length 388;
Best Local Similarity 100.0%; Pred. No. 2e-83;
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Db	127	AGTCCGACATGAAGGTGATCTGCAAGAGCTGCATCAGTCAAAACACCGGGGATAAATC	186
Qy	593	TGGATTTGGGTTCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACACTGTAAAATGC	652
Db	187	TGGATTTGGGTTCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACACTGTAAAATGC	246
Qy	653	CAGAAGCAGGTGAAGACACACCACCAAGTTTAAATGAAGACAACAGCTGAACACCCACAGCT	712
Db	247	CAGAAGCAGGTGAAGACACACCACCAAGTTTAAATGAAGACAACAGCTGAACACCCACAGCT	306
Qy	713	GGTTTATATTAGATATTTGACATTAAACTACTCTCAATAAAGTTTTCGACGCTTTTCACCAA	772
Db	307	GGTTTATATTAGATATTTGACATTAAACTACTCTCAATAAAGTTTTCGACGCTTTTCACCAA	366
Qy	773	AAA 775	
Db	367	AAA 369	
RESULT 20			
LOCUS BE620755 340 bp mRNA linear EST 20-OCT-2000			
DEFINITION 601483262T1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:388585 3', mRNA sequence.			
ACCESSION BE620755			
VERSION BE620755.1 GI:9891693			
KEYWORDS EST.			
SOURCE human.			
ORGANISM Homo sapiens			
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS NIH-MGC http://mgc.nci.nih.gov/			
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL Unpublished (1999)			
COMMENT Contact: Robert Strausberg, Ph.D. Email: crapbs-remail.nih.gov Tissue Procurement: DCTD/DTP/Gazdar cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9661 row: 1 column: 16 High quality sequence start: 26 High quality sequence stop: 340.			
FEATURES			
source 1..340			
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
/clone="IMAGE:388585"			
/clone_lib="NIH_MGC_69"			
/tissue_type="large cell carcinoma, undifferentiated"			
/lab_host="DH10B (phage-resistant)"			
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.1 kb. Library constructed by Life Technologies."			
BASE COUNT 57 a 86 c 78 g 119 t			
ORIGIN			
Query Match 30.9%; Score 241; DB 10; Length 340;			
Best Local Similarity 100.0%; Pred. No. 6.5e-77;			
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	408	GAACACACAGCCAGTCCCGAGGAGCCCGAGTAAATGGAGAGCCCGCCAAAAGAGAACACGACGA	467
Db	340	GAACACACAGCCAGTCCCGAGGAGCCCGAGTAAATGGAGAGCCCGCCAAAAGAGAACACGACGA	281
Qy	468	GCTGAAGTGGGATCCTACACCTGGCGACGACAGAGAAGATCAGGATACAGCTGAG	527
Db	280	GCTGAAGTGGGATCCTACACCTGGCGACGACAGAGAAGATCAGGATACAGCTGAG	221

Db 208 CAGAGCAGGTGAAGAGCAACCAAGCTTTAAATGAAGACAAAGCTGAACCAACGCAAGCT 267

QY 713 GCTTTTATTAGATATTGACTTAACTATCTCAATAAAGTTTTGGCAGCTTTCA 767
 |||||||
 Db 268 GCTTTTATTAGATATTGACTTAACTATCTCAATAAAGTTTTGGCAGCTTTCA 322
 |||||||

RESULT 22
 AW386187
 LOCUS
 DEFINITION RCO-PT0006-271199-011-E04 PT0006 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW386187
 VERSION AW386187.1 GI:8890846
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 230)
 HCGP http://www.ludwig.org.br/ORESTES.
 The FAPESP/LICR Human Cancer Genome Project
 Unpublished (1999)
 CONTACT Simpson A.J.G.
 LABORATORY Laboratory of Cancer Research
 LUDWIG Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC0&t2=RC0-PT0006-
 271199-011-E04&t3=1999-11-27&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 230.

FEATURES
 source
 1..230
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="PT0006"
 /dev_stage="Adult"
 /note="Organ: pnet; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No. 196
 ,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

BASE COUNT 78 a 52 c 65 g 35 t

ORIGIN
 Query Match 29.4%; Score 230; DB 9; Length 230;
 Best Local Similarity 100.0%; Pred. No. 7.3e-73;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 CCAGAGGCCAGTATGAGAGCCCCCAAAAAGAGAACCAACAGCTGAAAGTCGGGATC 483
 |||||||
 Db 1 CCCAGGAGCCAGTAAATGGAGAGCCCCCAAAAAGAGAACCAACAGCTGAAAGTCGGGATC 60
 |||||||

QY 484 CTACCTGGGACGACAGAGAGAGATCAGGATACAGCTCGAGATCCCGGCGACA 543
 |||||||
 Db 61 CTACCTGGGACGACAGAGAGAGATCAGGATACAGCTCGAGATCCCGGCGACA 120
 |||||||

QY 544 TGAAGGTGATCTGCAAGAGCTGCATCAGTCAAAACACCGGGGATAAATCTGGATTTGGGT 603
 |||||||
 Db 121 TGAAGGTGATCTGCAAGAGCTGCATCAGTCAAAACACCGGGGATAAATCTGGATTTGGGT 180
 |||||||

QY 604 TCCGGCGTCAAGGTGAAGATAATACCTAAAGAGGACACTGTAAATGCC 653
 |||||||
 Db 181 TCCGGCGTCAAGGTGAAGATAATACCTAAAGAGGACACTGTAAATGCC 230
 |||||||

RESULT 23
 AA642878
 LOCUS
 DEFINITION nu05H04.s1 NCI_CGAP_Alvl Homo sapiens cDNA clone IMAGE:1207159,
 mRNA sequence.
 ACCESSION AA642878
 VERSION AA642878.1 GI:2568096
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 318)
 NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
 Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 312.

FEATURES
 source
 1..318
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:1207159"
 /clone_lib="NCI_CGAP_Alvl"
 /tissue_type="alveolar rhabdomyosarcoma"
 /lab_host="DH10B"
 /note="vector: pAMP10; mRNA made from alveolar
 rhabdomyosarcoma, cDNA made by oligo-dT priming.
 Non-directionally cloned. Size-selected on agarose gel,
 average insert size 600 bp. Reference: Krizman et al.
 (1996) Cancer Research 56:5380-5383."

BASE COUNT 110 a 51 c 72 g 85 t

ORIGIN
 Query Match 29.4%; Score 230; DB 9; Length 318;
 Best Local Similarity 100.0%; Pred. No. 6.2e-73;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 533 AGTGGCCACATGGAAGGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATC 592
 |||||||
 Db 89 AGTGGCCACATGGAAGGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATC 148
 |||||||

QY 593 TGGATTTGGGTTCCGGCTCAAGGTGAAGATAATACCTAAAGAGAACACCTGTAATATGC 652
 |||||||
 Db 149 TGGATTTGGGTTCCGGCTCAAGGTGAAGATAATACCTAAAGAGAACACCTGTAATATGC 208
 |||||||

QY 653 CAGAAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGACAGCTGAACCAACCGCAAGCT 712
 |||||||
 Db 209 CAGAAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGACAGCTGAACCAACCGCAAGCT 268
 |||||||

QY 713 GGTTTTATTAGATATTGACTTAACTATCTCAATAAAGTTTTTGCAGC 762
 |||||||
 Db 269 GGTTTTATTAGATATTGACTTAACTATCTCAATAAAGTTTTTGCAGC 318
 |||||||

RESULT 24
 BG191783
 LOCUS
 DEFINITION RST10879 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION BG191783
 VERSION BG191783.1 GI:13713470
 KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1248)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,K., Smith
,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,k., Offenbacher
,J., Danzig,J. and Bucar,M.
Creation of genome-wide protein expression libraries using random
activation of gene-wide expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave. Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com
High quality sequence stop: 301.
Location/Qualifiers
1..1248
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="Hr1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is Hr1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in Hr1080 under normal circumstances."
BASE COUNT 291 a 278 c 257 g 401 t 21 others
ORIGIN
Query Match 27.4%; Score 214; DB 10; Length 1248;
Best Local Similarity 99.6%; Pred. No. 1.8e-67;
Matches 264; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 473 AAGTCGGGATCCCTACACCTGGGCAGCAGACAGAGAAGATCAGGATACAGCTGAGATCCC 532
|||||
Db 129 AAGTCGGGATCCCTACACCTGGGCAGCAGACAGAGAAGATCAGGATACAGCTGAGATCCC 188
QY 533 AGTCGGCGACATGAGAGGTGATCTGACAGAGCTGCATCAGTCAACACACCGGGGATAAATC 592
|||||
Db 189 AGTCGGCGACATGGAAGGTGATCTGCAAGAGCTGCATCAGTCAACACACCGGGGATAAATC 248
QY 593 TGGATTTGGGTTCCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACACTCTGAAATGC 652
|||||
Db 249 TGGATTTGGTTCGGCGCTCAAGGTGAAGATAATACCTAAAGAGGAACACTCTGAAATGC 308
QY 653 CACAAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGCAAGCTGAAACAACGCAAGCT 712
|||||
Db 309 CAGAAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGCAAGCTGAAACAACGCAAGCT 368
QY 713 GGTTTATATTAGATATTTGACTTA 737
|||||
Db 369 GGTTTATATTAGATATTTGACTTA 393
RESULT 25
AA412359
LOCUS 2199a04.r1 Soares_testis_NHT 299 bp mRNA linear EST 12-AUG-1997
DEFINITION 5', mRNA sequence.
ACCESSION AA412359
VERSION AA412359.1 GI:2070929
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 299)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie
,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
JOURNAL
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 503 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 256.
Location/Qualifiers
1..299
/organism="Homo sapiens"
/db_xref="GDB:5927024"
/db_xref="taxon:9606"
/clone="IMAGE:73046"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 86 a 83 c 88 g 42 t
ORIGIN
Query Match 26.2%; Score 205; DB 9; Length 299;
Best Local Similarity 100.0%; Pred. No. 6.5e-64;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 392 GACACACAAACACAGAACACACAGCAGTCCAGAGCCCGCCAGATGGAGAGCCCA 451
|||||
Db 95 GACACACAAACACAGAACACACAGCAGTCCAGAGCCCGCCAGATGGAGAGCCCA 154
QY 452 AAAAGAAGAACACAGCAGCTGAAAGTCGGGATCCTACACCTGGGCAGCAGACAGAAGA 511
|||||
Db 155 AAAAGAAGAACACAGCAGCTGAAAGTCGGGATCCTACACCTGGGCAGCAGACAGAAGA 214
QY 512 TCAGGATACAGCTGAGATCCCCAGTCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCA 571
|||||
Db 215 TCAGGATACAGCTGAGATCCCCAGTCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCA 274
QY 572 GTCAAACACCGGGGATAAATCTGGA 596
|||||
Db 275 GTCAAACACCGGGGATAAATCTGGA 299
RESULT 26
AA747475
LOCUS nx73C03.s1 NCL_CCAP_Ew1 229 bp mRNA linear EST 07-FEB-1998
DEFINITION sequence.
ACCESSION AA747475
VERSION AA747475.1 GI:2787433
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 229)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-i@mail.nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 429 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 200.
FEATURES
source 1..229
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1267876"
/clone_lib="NCI-CGAP-Ew1"
/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
/note="Vector: pAMP10; mRNA made from Ewing's sarcoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
BASE COUNT 80 a 48 c 65 g 36 t
ORIGIN
Query Match 24.8%; Score 194; DB 9; Length 229;
Best Local Similarity 100.0%; Pred. No. 6.8e-60; Indels 0; Gaps 0;
Matches 194; Conservative 0; Mismatches 0;
QY 463 CAGCAGCTGAAAGTCGGGATCCTACCTGGCGCAGCAGACAGAAAGATCAGGATACAG 522
|||||
Db 36 CAGCAGCTGAAAGTCGGGATCCTACCTGGCGCAGCAGACAGAAAGATCAGGATACAG 95
QY 523 CTGAGATCCCGAGTCGGCGACATGGAAGTGATCTGCAAGAGCTGCATCAGTCAACACCG 582
|||||
Db 96 CTGAGATCCCGAGTCGGCGACATGGAAGTGATCTGCAAGAGCTGCATCAGTCAACACCG 155
QY 583 GGGATAAATCTGGATTTCGGTTCGGCGCTCAAGGTGAAGATAATACCTAAAGAGCAACAC 642
|||||
Db 156 GGGATAAATCTGGATTTCGGTTCGGCGCTCAAGGTGAAGATAATACCTAAAGAGCAACAC 215
QY 643 TGTAAATGCCAGA 656
|||||
Db 216 TGTAAATGCCAGA 229
RESULT 27
BG193320
LOCUS BG193320 407 bp mRNA linear EST 21-APR-2001
DEFINITION RST12448 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG193320
VERSION BG193320.1 GI:13715007
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 407)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith , E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher ,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random

activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 407.
FEATURES
source 1..407
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/clone_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT 152 a 85 c 97 g 73 t
ORIGIN
Query Match 24.3%; Score 190; DB 10; Length 407;
Best Local Similarity 100.0%; Pred. No. 1.4e-58; Indels 0; Gaps 0;
Matches 190; Conservative 0; Mismatches 0;
QY 535 TGGCGACATGGAAGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAATCTG 594
|||||
Db 160 TGGCGACATGGAAGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAATCTG 219
QY 595 GATTGGTTCGGCGCTCAAGGTGAAGATAATACCTAAAGAGCAACACTGTAAATGCCA 654
|||||
Db 220 GATTGGTTCGGCGCTCAAGGTGAAGATAATACCTAAAGAGCAACACTGTAAATGCCA 279
QY 655 GAAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGACAAGCTGAACACGCAAGCTGG 714
|||||
Db 280 GAAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGACAAGCTGAACACGCAAGCTGG 339
QY 715 TTTTATATTA 724
|||||
Db 340 TTTTATATTA 349
RESULT 28
BG221249
LOCUS BG221249 409 bp mRNA linear EST 21-APR-2001
DEFINITION RST41052 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG221249
VERSION BG221249.1 GI:13747270
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 409)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith , E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher ,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 409.

FEATURES
source High quality sequence stop: 409.
Location/Qualifiers
1..409

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT 153 a 86 c 97 g 73 t
ORIGIN

Query Match 24.3%; Score 190; DB 10; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 535 TCGCGCACATGAAGGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATCTG 594
DB 162 TCGCGCACATGAAGGTGATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATCTG 221
QY 595 GATTGGGTTCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACACTGTAAAATGCCA 654
DB 222 GATTGGGTTCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACACTGTAAAATGCCA 281
QY 655 GAAGCAGGTGAAGACCAACCAAGTTTAAATGAAGACAGCTGAACCAACCGAAGCTGG 714
DB 282 GAAGCAGGTGAAGACCAACCAAGTTTAAATGAAGACAGCTGAACCAACCGAAGCTGG 341
QY 715 TTTTATATTA 724
DB 342 TTTTATATTA 351

RESULT 29
AA483341/c
LOCUS ne64h05.s1 NCI_CGAP_Alvl Homo sapiens cDNA clone IMAGE:909081, mRNA
DEFINITION sequence.
ACCESSION AA483341
VERSION AA483341.1 GI:2212154
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 289)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 495 Std Error: 0.00
Seq primer: -41m3 fwd. ET from Amersham
High quality sequence stop: 279.
Location/Qualifiers
1..289

FEATURES
source /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:909081"
/clone_lib="NCI_CGAP_Alvl"

/tissue_type="alveolar rhabdomyosarcoma"
/lab_host="DH10B"
/note="Vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma, cDNA made by oligo-dT priming. Non-directionally cloned. Size selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
BASE COUNT 77 a 63 c 47 g 102 t
ORIGIN

Query Match 24.2%; Score 189; DB 9; Length 289;
Best Local Similarity 100.0%; Pred. No. 3.8e-58;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 533 AGTGGCGACATGGGAAGGTGATCTGCAAGAGCTGCATCAACACCGGGGATAAATC 592
DB 240 AGTGGCGACATGGGAAGGTGATCTGCAAGAGCTGCATCAACACCGGGGATAAATC 181
QY 593 TGGATTGGTTCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACACTGTAAAATGC 652
DB 180 TGGATTGGTTCGGCGTCAAGGTGAAGATAATACCTAAAGAGGAACACTGTAAAATGC 121
QY 653 CAGAAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGACAGCTGAACACAGCGAAGCT 712
DB 120 CAGAAGCAGGTGAAGAGCAACCAAGTTTAAATGAAGACAGCTGAACACAGCGAAGCT 61
QY 713 GGTTTTATA 721
DB 60 GGTTTTATA 52

RESULT 30
AA730288
LOCUS nw41c01.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1249152, mRNA
DEFINITION sequence.
ACCESSION AA730288
VERSION AA730288.1 GI:2751492
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 202)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 281 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
Location/Qualifiers
1..202

FEATURES
source /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:1249152"
/clone_lib="NCI_CGAP_Ew1"
/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
/note="Vector: pAMP10; mRNA made from Ewing's sarcoma. cDNA made by oligo-dT priming. Non-directionally cloned. Size selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

```

BASE COUNT      79 a      34 c      41 g      48 t
ORIGIN
Query Match      22.2%; Score 173; DB 9; Length 202;
Best Local Similarity 100.0%; Pred. No. 2.7e-52;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 GCGTCAGGTGAAGATTAATACCTAAAGAGGAACACTGTAAATGCCAGAGCAGGTGAA 666
DB 23 GCGTCAGGTGAAGATTAATACCTAAAGAGGAACACTGTAAATGCCAGAGCAGGTGAA 82
QY 667 GAGCAACACAAAGTTTAAATGAAGACAAGCTGAAACAACGCAAGCTGGTTTATATTAGA 726
DB 83 GAGCAACACAAAGTTTAAATGAAGACAAGCTGAAACAACGCAAGCTGGTTTATATTAGA 142
QY 727 TATTTGACTTAAACTATCTCAATTAAGTTTTCAGCTTTTCCACCAAAAAA 779
DB 143 TATTTGACTTAAACTATCTCAATTAAGTTTTCAGCTTTTCCACCAAAAAA 195

RESULT 31
A1205793/c      291 bp      mRNA      linear      EST 29-NOV-1998
LOCUS      qg33b06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1836947
DEFINITION      3', mRNA sequence.
ACCESSION      A1205793
VERSION      A1205793.1 GI:3764465
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 291)
AUTHORS      NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaide
, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 555 Std Error: 0.00
Seq primer: -40Up from Gibco
High quality sequence stop: 248.
Location/Qualifiers
1. .291
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1836947"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - Oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGCGCGCCCAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaide."
BASE COUNT      60 a      68 c      52 g      111 t
ORIGIN
Query Match      22.2%; Score 173; DB 9; Length 291;
Best Local Similarity 99.3%; Pred. No. 2.2e-52;
Matches 273; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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QY 493 GGCAGCAGACAGAAGAAGATCAGGATACAGCTCAGATCCAGTCCGCGACATGAAAGGTG 552
DB 290 GGCAGCAGACAGAAGAAGATCAGGATACAGCTCAGATCCAGTCCGCGACATGAAAGGTG 231
QY 553 ATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATCTGGATTGGTTCCGGCGTC 612
DB 230 ATCTGCAAGAGCTGCATCAGTCAACACCGGGGATAAATCTGGATTGGTTCCGGCGTC 171
QY 613 AAGTGAAGATAATACCTAAAGAGGAACACTGTAAATGCCAGAAGCAGGTGAAGAGCAA 672
DB 170 AAGTGAAGATAATACCTAAAGAGGAACACTGTAAATGCCAGAAGCAGGTGAAGAGCAA 111
QY 673 CCACAAGTTTAAATGAAGACAAGCTGAAACAACGCAAGCTGGTTTATATTAGATATTG 732
DB 110 CCCCAAGTTTAAATGAAGACAAGCTGAAACAACGCAAGCTGGTTTATATTAGATATTG 51
QY 733 ACTTAACTATCTCAATTAAGTTTTCAGCTTTCA 767
DB 50 ACTTAACTATCTCAATTAAGTTTTCAGCTTTCA 16

RESULT 32
BG211375      487 bp      mRNA      linear      EST 21-APR-2001
LOCUS      RST30937 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
DEFINITION      BG211375
ACCESSION      BG211375
VERSION      BG211375.1 GI:13733062
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 487)
AUTHORS      Hall, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,
Cain, S., Leventhal, C., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith
, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher
, J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
JOURNAL      21227151
MEDLINE
COMMENT      Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 343.
Location/Qualifiers
1. .487
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/clone_line="HT1080"
/notes="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression', the
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT      169 a      100 c      127 g      91 t
ORIGIN
Query Match      20.9%; Score 163; DB 10; Length 487;
Best Local Similarity 99.2%; Pred. No. 6.9e-49;
Matches 263; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 392 GACACACAAACACACACACACAGCCAGTCCCGAGGCCAGTAAATGAGAGCCCCA 451
DB 94 GACACACAAACACACACACACAGCCAGTCCCGAGGCCAGTAAATGAGAGCCCCA 153


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QY 452 AAAAGAACACCACGCTGAAAGTCCGGATCCTACACCTGGGCAGCAGACAGAGAAGA 511
Db 154 AAAAGAAAGACGACGCTGAAAGTCCGGATCCTACACCTGGGCAGCAGACAGAGAAGA 213

QY 512 TCAGGATACAGCTGAGATCCCGAGTCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCA 571
Db 214 TCAGGATACAGCTGTTATCCAGTCGCGACATGGAAGGTGATCTGCAAGAGCTGCATCA 273

QY 572 GTCAAACACCGGGGATAAATCTGATTGGTTCCGGGTCGCAAGGTGAAGATAATACCTA 631
Db 274 GTCAAACACCGGGGATAAATCTGATTGGTTCCGGGTCGCAAGGTGAAGATAATACCTA 333

QY 632 AAGAGGAACACTGTAATAATGCCAGA 656
Db 334 AAGAGGAACACTGTAATAATGCCAGA 358

RESULT 33
LOCUS BG205627 391 bp mRNA linear EST 21-APR-2001
DEFINITION RST25074 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG205627
VERSION BG205627.1 GI:13727330
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 391)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com
High quality sequence stop: 391.
FEATURES
source
1..391
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
Note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 144 a 84 c 90 g 73 t
ORIGIN
Query Match 19.5%; Score 152; DB 10; Length 391;
Best Local Similarity 100.0%; Pred. No. 7.1e+45;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 GAAGATCAGGATACAGCTGAGATCCAGTCGCGACATGGAAGGTGATCTGCAAGAGCTG 566
Db 115 GAAGATCAGGATACAGCTGAGATCCAGTCGCGACATGGAAGGTGATCTGCAAGAGCTG 174

QY 567 CATCAGTCAAAACACCGGGGATAAATCTGGATTTCGGGTCGCAAGGTGAAGATAAT 626
Db 175 CATCAGTCAAAACACCGGGGATAAATCTGGATTTCGGGTCGCAAGGTGAAGATAAT 234

QY 627 ACCTAAGAGGAACACTGTAATAATGCCAGAAG 658
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Db 235 ACCTAAGAGGAACACTGTAATAATGCCAGAAG 266

RESULT 34
LOCUS AW386180 195 bp mRNA linear EST 04-FEB-2000
DEFINITION RC0-PT0006-271199-011-A08 PT0006 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW386180
VERSION AW386180.1 GI:6890839
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 195)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC0&t2=RC0-PT0006-
271199-011-A08&t3=1999-11-27&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 195.
FEATURES
source
1..195
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="PT0006"
/dev_stage="Adult"
Note="Organ: pnet; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 69 a 50 c 56 g 20 t
ORIGIN
Query Match 18.3%; Score 143; DB 9; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.8e+41;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 GACACACAAAACACAGAACACACAGCCAGTCCAGAGAGCCAGTAATGGAGAGCCCA 451
Db 12 GACACACAAAACACAGAACACACAGCCAGTCCAGAGAGCCAGTAATGGAGAGCCCA 71

QY 452 AAAAGAAAGAACACGACGCTGAAAGTCCGGATCCTACACCTGGGCAGCAGACAGAGAAGA 511
Db 72 AAAAGAAAGAACACGACGCTGAAAGTCCGGATCCTACACCTGGGCAGCAGACAGAGAAGA 131

QY 512 TCAGGATACAGCTGAGATCCCAAG 534
Db 132 TCAGGATACAGCTGAGATCCCAAG 154

RESULT 35
LOCUS AW386185 195 bp mRNA linear EST 04-FEB-2000
DEFINITION RC0-PT0006-271199-011-D10 PT0006 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW386185
VERSION AW386185.1 GI:6890844
KEYWORDS EST.
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SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195)
AUTHORS HCGP <http://www.ludwig.org.br/ORESITES>.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?L1=RC0&L2=RC0-PT0006-271199-011-D10&t3=1999-11-27&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 195.
Location/Qualifiers
1..195
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="PT0006"
/dev_stage="Adult"
/note="Organ: pnet; Vector: puc18; Site1: Small; Site2:
Small; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 69 a 50 c 56 g 20 t
ORIGIN
Query Match 18.3%; Score 143; DB 9; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.8e-41;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 392 GACACACACACACACAGACACAGCCAGTCCAGGAGCCAGTAATGGAGAGCCCA 451
Db 12 GACACACACACACACAGACACACAGCAGTCCAGGAGCCAGTAATGGAGAGCCCA 71
QY 452 AAAAGAGAACACGACGCTGAAAGTCGGATCCTACACCTGGGCGACGACAGAGAAGA 511
Db 72 AAAAGAGAACACGACGCTGAAAGTCGGATCCTACACCTGGGCGACGACAGAGAAGA 131
QY 512 TCAGGATACAGTCGATCCAG 534
Db 132 TCAGGATACAGTCGATCCAG 154
RESULT 36
BG205090
LOCUS BG205090 389 bp mRNA linear EST 21-APR-2001
DEFINITION BST24509 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
ACCESSION BG205090
VERSION BG205090.1 GI:13726777
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 389)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random

activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
2127151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 389.
Location/Qualifiers
1..389
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 141 a 78 c 97 g 72 t
ORIGIN
Query Match 17.8%; Score 139; DB 10; Length 389;
Best Local Similarity 99.5%; Pred. No. 3.4e-40;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 535 TCGCGACATGAAGTGATCTGCAAGAGCTGCATCAACACCGGGGATAATCTG 594
Db 142 TCGCGACATGAAGTGATCTGCAAGAGCTGCATCAACACCGGGGATAATCTG 201
QY 595 GATTTGGGTTCGGCGCTCAAGGTGAAGTAATACCTAAAGAGGAACACTGTAAATGCCA 654
Db 202 GATTTGGGTTCGGCGCTCAAGGTGAAGTAATACCTAAAGAGGAACACTGTAAATGCCA 261
QY 655 GAAGCAGGTGAAGAGCAACCAACGATTTAAATGAAGACAAGCTGAACACCAAGCTGG 714
Db 262 GAAGCAGGTGAAGAGCAACCAACGATTTAAATGAAGACAAGCTGAACACCAAGCTGG 321
QY 715 TTTTATATTA 724
Db 322 TTTTATATTA 331
RESULT 37
T19106
LOCUS T19106 324 bp mRNA linear EST 25-SEP-1996
DEFINITION D01019T Testis 1 Homo sapiens CDNA clone D01019 5' end, mRNA
sequence.
ACCESSION T19106
VERSION T19106.1 GI:601149
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 324)
Pawlak,A., Toussaint,C., Levy,I., Bulle,F., Poyard,M., Barouki,R.
and Guellaen,G.
TITLE Characterization of a large population of mRNAs from human testis
JOURNAL Genomics 26, 151-158 (1995)
MEDLINE 95301283
COMMENT Contact: Guellaen G
Unite INSERM 99
INSERM
Unite INSERM 99, Hopital Henri Mondor, 94010 Creteil, France
Tel: (33)149813530
Fax: (33)14980908
Email: guellaen@infobiogen.fr
Seq primer: T7.
Location/Qualifiers

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source
1. .324
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="p01019"
/clone_lib="Testis 1"
/note="Vector: pGEM 5zf(+); Site_1: EcoRV; Site_2: NotI;
mRNA was prepared from human testis of a 27 years old man.
cDNA was prepared using a 15mer oligo dt anchored by two
degenerated bases at its 3'end and containing a NotI site
at its 5'end. The cDNA was cloned between EcoRV and NotI
sites of pGEM 5zf(+). The 3' end is at the NotI site. The
EcoRV site is lost during the cloning procedure. cDNA
corresponding to abundant species were eliminated from
this library."
BASE COUNT      92 a      81 c      95 g      50 t      6 others
ORIGIN
Query Match      16.0%; Score 125; DB 10; Length 324;
Best Local Similarity 100.0%; Pred. No. 4.2e-35;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 GACACACAAACACAGAACACACAGCCAGTCCCGAGGCCAGTAATGGAGAGCCCA 451
      |||||||
Db 88 GACACACAAACACAGAACACACAGCCAGTCCCGAGGCCAGTAATGGAGAGCCCA 147

QY 452 AAAAGAAGACCAGCAGCTGAAAGTCGGGATCTACACCTGGCGCAGCAGACAGAAGA 511
      |||||||
Db 148 AAAAGAAGACCAGCAGCTGAAAGTCGGGATCTACACCTGGCGCAGCAGACAGAAGA 207

QY 512 TCAGG 516
      |||||
Db 208 TCAGG 212

RESULT 38
AW386181/c
LOCUS      AW386181      132 bp      mRNA      linear      EST 04-FEB-2000
DEFINITION RC0-PT0006-271199-011-A08_1 PT0006 Homo sapiens cDNA, mRNA
sequence.
ACCESSION  AW386181
VERSION    AW386181.1 GI:6890840
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 132)
            HGCP http://www.ludwig.org.br/ORESTES.
            The FAPESP/LICR Human Cancer Genome Project
            Unpublished (1999)
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC0&t2=RC0-PT0006-
            271199-011-A08_1&t3=1999-11-27&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 132.
            Location/Qualifiers
                1. .132
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="PT0006"
                /dev_stage="Adult"
                /note="Organ: pnet; Vector: puc18; Site_1: SmaI; Site_2:
                SmaI; A mini-library was made by cloning products derived
                from ORESTES PCR (U.S. Letters Patent application No. 196
```

```
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT      10 a      33 c      38 g      51 t
ORIGIN
Query Match      15.5%; Score 121; DB 9; Length 132;
Best Local Similarity 100.0%; Pred. NO. 1.8e-33;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 GACACACAAACACAGAACACACAGCCAGTCCCGAGGCCAGTAATGGAGAGCCCA 451
      |||||||
Db 121 GACACACAAACACAGAACACACAGCCAGTCCCGAGGCCAGTAATGGAGAGCCCA 62

QY 452 AAAAGAAGACCAGCAGCTGAAAGTCGGGATCTACACCTGGCGCAGCAGACAGAAGA 511
      |||||||
Db 61 AAAAGAAGACCAGCAGCTGAAAGTCGGGATCTACACCTGGCGCAGCAGACAGAAGA 2

QY 512 T 512
      |
Db 1 T 1

RESULT 39
BG208252
LOCUS      BG208252      406 bp      mRNA      linear      EST 21-APR-2001
DEFINITION R527744 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG208252
VERSION    BG208252.1 GI:13729939
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 406)
            Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
            Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
            Creation of genome-wide protein expression libraries using random
            activation of gene expression
            Nat. Biotechnol. 19 (5), 440-445 (2001)
            2127151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 406.
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Qy 534 G 534
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Db 142 G 142

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VERSION AW386186.1 GI:6890845
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 132)
AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL:
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC0&t2=RC0-PT0006-271199-011-D10.1&t3=1999-11-27&t4=1>)
Seq primer: puc 18 forward
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FEATURES
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,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
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Db 121 GACACACAAACACAGAACACACAGCCAGTCCCGAGGAGCCAGTAATGGAGAGCCCA 62
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Qy 452 AAAAGAGAACCAGCAGCTGAAGTGGGATCCTACACCTGGGCAGCAG 500
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Search completed: October 16, 2002, 23:00:45
Job time : 1617 secs